'STIC-Biotech/ChemLib

34254

From:

Chan, Christina

Sent: T : Subject: Tuesday, January 14, 2003 3:04 PM Yu, Misook; STIC-Biotech/ChemLib RE: rush search for 09/648,310

Importance:

High

Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message----

From: Yu, Misook

Sent: Tuesday, January 14, 2003 11:43 AM

To: Chan, Christina

Subject:

rush search for 09/648,310

Please approve rush searh. The case is due this bi-week.

Please search SEQ ID NO:1 and 2.

Examiner Misock YUN Phy 703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

Chia

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: /36/3
Phone:
Location:
Date Picked Up:
Date Completed: 1-17-03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

BioTech-Chem Library Search Results Feedback Form (Optional)



The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact the BioTech-Chem searcher who conducted the search or contact:

Mary Hale, Supervisor, 308-4258 CM-1 Room 1E01

Volu	ntary Results Feedback Form
>	I am an examiner in Workgroup: (Example: 1610)
>	Relevant prior art found, search results used as follows:
	102 rejection
	103 rejection
•	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Search results were not useful in determining patentability or understanding the invention.
Other	· Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or mary.hale@uspto.gov

Yu, Misook

To:

Chan, Christina

Subject:

rush search for 09/648,310

Please approve rush searh. The case is due this bi-week.

Please search SEQ ID NO:1 and 2.

Examiner Misook Yu, Ph.D. 703-308-2454 (Phone) Art Unit 1642 CM1-8E18 (Room) CM1-8E12 (Mail Box)

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

January 16, 2003, 21:46:28; Search time 102 Seconds Run on:

(without alignments) 3409.581 Million cell updates/sec

1 ggcacgagctctcctcgtcc......gtaataaaaaaaaatcatgt 780 US-09-648-310-1 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

393868 seqs, 222934149 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PC07_ENRW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/NS06_BUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/2/pubpna/US08_BUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/70509_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/70500_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Query	Query Match Length DB	DB	ID	Description
-	288.2	36.9	778	10	TS-09-905-300-848	
~	206.6	26.5	4.5	1 -	0.00 -0.00 -0.00	seduence 545, App
۰ ۱	3000		9 10	1 .	US-US-920-30UA-939	Sequence 939, App
η.	2007	70.0	252	12	US-10-033-528-939	Sequence 939. App
₹ 1	122.4	15.7	388	10	US-09-925-299-318	310
Ŋ	109.6	14.1	486	σ	US-09-938-842A-355	Cognopolo SEE
9	95.8	11.9	365	σ	118-10-046-935-2101	Sequence 355, App
7	92.8	11 9	36.5	σ	NS-00-070-170-2101	de 'Ini anna
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•	7.70	0.11	400	7		Sequence 687. April
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10	63.2	8.1	289	10	US-09-294-093B-4150	Segmence Alfo
11	38.6	4.9	6222	6	_	de 'acres 4130' Ap
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7	8	4.9	2000	0	US-09-938-842A-3235	Sequence 3235 An
14	37.6	4.8	338	6	US-10-046-935-342	Spellenge 340
15	37.6	4.8	338	σ	TIG-00-878-178-07-	ddy '7*c annana
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7	37.6	4.8	1967	10	US-09-925-301-565	
18	37.6	4.8	2431	10	US-09-822-830A-395	ddy /coc powertos
13	37	4.7	2000	σ	TIS-00-038-8428-4612	
)	,	2TO# U7#0 000 00	seduence 4p17. An

	Sequence 1, Appli	Sednence I, Appl1	seguence 4/32, Ap	Sequence 912. App		Company 187	ddy '/cr annanhac	ddw '128' App	Sequence 3392, Ap	Sequence 2, Appli	Segmence 3. April	Socionos	מלתפווכם זי שההדד	sedneuce II2/, Ap	Sequence 605, App	Segmence 605 Ann	Section Source Section 1973	Socionary A	de '2' 'E' Ap	sedneuce /// Appl	Sequence 314, App	Segmence 4264 An	Segmence 15014	d troct concerns	Seducince 4' Appli	Sequence 117, App	Sequence 131. App	Sequence 1. Appli	Segmence 4572 An	Sequence 3707, Ap
119-00-813-742-1	T 2 1 2 2 2 2 2 1 1 1 1 1 2 2 2 2 2 2 2	T 007 077 70 02	25 / 5-828-05 CO	US-09-969-373-912	US-09-969-373-913	US-09-754-853A-157	TG+00-754-8533-159	TC-00-030-073-330	26.50 - 04.24 - 3.39.2	US-09-754-853A-2	US-09-754-853A-3	US-09-739-457-5	115-00-060-372-1167	10 10 012 010 010 CD	US-IO-015-219-605	US-09-777-564-605	US-09-864-761-20733	US-09-864-761-3972	HG-10-114-003-77	//-C20 TTT 07 CO	US-10-114-893-314	US-09-938-842A-4264	US-09-960-352-15014	US-09-754-8534-4	F 1100 - 070 - 00 - 011	/TT-700-706-60-CO	US-09-867-701-131	US-09-790-988-1	US-09-878-574-4572	US-09-938-842A-3707
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ALIGNMENTS

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                                                                                                           TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA101
                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 545
LENGTH: 778
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (641)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (652)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-545
               Sequence 545, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-925-300-545
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APPLICANT: King, Gordon E.
APPLICANT: Maedleine Joy
APPLICANT: Waedleine Joy
APPLICANT: Waedleine Joy
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION: WUMBER: US/09/920,300A
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 206.6; DB 10; Length 552;
Pred. No. 4e-46;
); Mismatches 144; Indels 23;
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Best Local Simi
Matches 366;
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LENGTH: 552
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                                                                                                                   133 TTTGTTCATAAATAATTAGACATTTTCTATAGATATTTGACATTCTGCGAAAGCAACAAG
                                  --TCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---GAAGTTCC
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                                                  CATTITITGTITCTGGTAAACTGGAAT-ATAAAGTGAAAGAACAAACATTGAACATACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 939, Application US/10033528

| Patent No. US20020131971a1
| GENERAL Information:
| APPLICANT: King, Gordon E. |
| APPLICANT: King, Gordon E. |
| APPLICANT: King, Jangchun |
| APPLICANT: Secrist, Heather |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER |
| FILE REFERENCE: 210121.547C1 |
| CURRENT APPLICATION NUMBER: US/10/033,528 |
| CURRENT FILING DATE: 2001-12-26 |
| NUMBER OF SEQ ID NOS: 1896 |
| SOFTWARRE: FastSEQ for Windows Version 4.0 |
| SOFTWARRE: FastSEQ for Windows Version 4.0 |
                                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 552;
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Pred. No. 4e-46;
0; Mismatches 144;
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Best Local Similarity 68.7%;
Matches 366; Conservative
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CORGANISM: Homo sapiens
US-10-033-528-939
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                                                                                                                                                      TTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTT 662
                                                                                                                                                                                                                                                                                                             663 TGTTTTCTTAAACCATTCTTAGTCT--CTGCCACACTTGACACTCCGTCAAAGTGAGAAG 720
APPLICANT: Rosen et al.

TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 318
LENTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
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LOCATION: (143)
OTHER INFORMATION: n equals a,t,g, or
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NAME/KEY: misc_feature
LOCATION: (144)
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LOCATION: (146)
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OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 318, Application US/09925299
Patent No. US20020055627Al
GENERAL INFORMATION:
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LOCATION: (2)
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LOCATION: (159)
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LOCATION: (163)
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169 AATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGAAATTCATCGTCTGGGTTCCAA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.7%; Score 122.4; DB 1
65.8%; Pred. No. 1.4e-23;
live 0; Mismatches 81
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CATER INFORMATION: n equals a,t,g, or c
US-09-928-299-318
                                                                                                                                                                                                                                                                                                                    LOCATION: (223)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (234)
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g, or
                                                                                                                  or
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LOCATION: (198)
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                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n equals a, t, g, or
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
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INFORMATION: n equals a,t,g, or
                                                      OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
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                                                                                                            OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                 OTHER INFORMATION: n equals
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Best Local Similarity 65.8
Matches 156; Conservative
                                                                                                                              NAME/KEY: misc_feature
LOCATION: (174)
                       : misc_feature
                                                                                                                                                                                    NAME/KEY: misc_feature
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436 GIATCTGGTAAACTGGAATAATTAAGGTAAAGGACAAACAT---GAAGTTCCTTATGTAT 492
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                                                                                                                                                                                                                                                                                                                         671 TAAACCATTCTTAGTCT - - CTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAA 728
                                                                                                                                                                                                                                             GTATCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---GAAGTTCCTTATGTAT 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          611 GTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCT
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                                                                                                                                          Length 365;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2101. Application US/09878178
Patent No. US2002017552A1
GENERAL INFORMATION:
APPLICANT: Jang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE T
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SEQ ID NO 2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 92.8; DB 9; 1
Pred. No. 1.3e-15;
0; Mismatches 123;
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llarity 62.0%; Pred. No. 1.3e-15;
Conservative 0; Mismatches 123;
                                                        ; LOCATION: 273
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(365)
; OTHER INFORMATION: n - A,T,C or G
US-09-878-178-2101
                                                                                                                                      11.9%;
62.0%;
                                                                                                                                    Query Match 11.99
Best Local Similarity 62.09
Matches 214; Conservative
ORGANISM: Homo sapiens
                                     NAME/KEY: misc_feature
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                                                                                                                                                                 APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US /09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGAACGTAGACGAAGAGATTCAGAAACTGGAAGAAGAGATCCATCGTCTTGGTTCTCG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
            320 CAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGTNAAACGANANAAGAATGT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 AAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC
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Patent No. US20020156011a1
GENERAL INFORMATION:
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACGCAGGAGACCTGCTTTTGCAAGGTGTTCATGATGATGTTGACAT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 109.6; DB 9
Pred. No. 4.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 210121.527C1
CURRENT PELLING NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2101
LENGTH: 365
                                                                                                                                  Sequence 355, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Arabidopsis thaliana US-09-938-842A-355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
14.1%;
Best Local Similarity 67.5%;
Matches 154; Conservative
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Best Local Similarity
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                                                                                            RESULT 5
US-09-938-842A-355
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GTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAAGCTTTTGTTTTCT 670
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                                      233 TCTTGAAAGAAAATCTATGTATGATGCTATAAAATAAATCCTATTATTTTTCTCAGGAAT 174
                                                                                                         436 GTATCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---GAAGTTCCTTATGTAT 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA287347
US-09-880-107-687
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 687, Application US/09880107

Sequence 687, Application US/09880107

Patent No. US20020142981A1

Seduence INFORMATION:

APPLICANT: HORNE, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TILE REFERENCE: 44921-5028-WO

CURRENT FAPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PATENTIN VEY: 2.1

LENGTH: 406
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                                                                                                                                                                                                                                               729 AGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAAA 773
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Matches 214; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700353201H1
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LOCATION: 9, 111, 148, 231, 265, 286
OTHER INFORMATION: a, t, c, g, or other
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ORGANISM: Zea mays
RESULT 10
US-09-294-093B-4150
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                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 4150
LENGTH: 289
                                                                                                                                                         261 TCTTGAAAGAAAATCTATGATGATGATAAAAAAAAAACCTATTATTTTCTCAGGAAT 202
                                                                                                                                                                                                                                                                                                                                                                          201 CIGGITAGGAATIGCAGGCAAIGAGATITITIGCGGGCAGGGAIGGGAAIGTITGITCA 142
                                                                                                                                                                                                                                                                                                                                                                                                                         671 TAAACCATTCTTAGTCT--CTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAA 728
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                                                                                                                                                                                                                            611 GTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCT
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729 AGACCAACTGCGGTGGAAAATATTATGTTTATGTAATAAAAAA 773

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Sequence 2020, Application US/09294093B

Patent No. US20010051335A1

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Sherman, Bradley, K.
TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT FILING DATE: 1999-04-16
PRIOR PILING DATE: 1999-04-16
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SEQ ID NO 2020
LENGTH: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4150, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT: Lalqudi, Raghunath, V.
APPLICANT: Sherman, Bradley, K.
TILLE OF INVENTION:
POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL:
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR FILING DATE: APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: APPLI 21, 1998
NUMBER OF SEQ ID NOS: 6207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 268;
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; OTHER INFORMATION: Incyte ID No. US20010051335A1 700345395H1
US-09-294-093B-2020
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Best Local Similarity 65.8%; Pred. No. 3.1e-14;
Matches 127; Conservative 0; Mismatches 66;
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US-09-294-093B-2020
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Yun
APPLICANT: The Mang, Yun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILLE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4123 TTATTTTTAAAACCGTCCAATACCTTTTGTATTATGTAACATTCAAAAGACAATGTACTG 4182
                          4003 GTAAATACTATTTAATGAACGACTGTACAAAGTAGAATTCCTAGATGTATTTTTGTATG 4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 GTAAACTGGAATAATTAAGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTATAGAC 502
517 GGGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACATTACAATGTAAAAAT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTTTATACCTTGGAGCAAAACAT
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                                                                                                                                                                                                                                                                                                                methods to inhibit or
                                                                                                                                                                                                                                                               APPLICANT: Grainger, David J.
APPLICANT: Grainger, Lauen Marie
TITLE OF INVENTION: Compounds and methods to inhibit of TITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 295.022031
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT FILING DATE: 1997-09-11
NUMBER OF EXQ ID NOS: 83
SOFTHARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11arity 48.6%; Score 38.4; DB 8;
12arity 48.6%; Pred. No. 1.8;
Conservative 0; Mismatches 111;
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                                                                                                                                                                                                        Sequence 30, Application US/08927939; Patent No. US20010006640al; GENERAL INFORMATION:
                                                                                               3631 ATACAAAACCAGTTATTGCTT 3611
                                                                         577 AAACAAAACCTGTTATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS (2070) ... (2130)
CDS (2669) ... (2795)
CDS (2089)
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; NAME/KEY: CDS
; LOCATION: (3491)...(3506)
US-08-927-939-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
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Matches 105; Conservat
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US-08-927-939-30
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LOCATION:
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NAME/KEY:
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Best Local
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                                                                                                                                                                    AAAAATGCCGATGGGAAACTGGAGTGTGAGGTTTGGGGTCCTCTTCCAAGACGACAGAGTGT.286
                                                                                                                                                                                                                                                 136 CAGCAGCCCGAINGCICITACAAGGICAAGTITGGCGTICITCTAAACGACGATCGGTGI 195
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                  Length 289;
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TITLE OF INVENTION: No. US20020197679Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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                                                      Indels
                      7;
1e-07;
82;
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            8.1%; Score 63.2; DB 10;
ilarity 59.3%; Pred. No. 1e-07;
Conservative 0; Mismatches 82;
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Pred. No. 1.9;
0; Mismatches 64;
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PRIOR PELICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR PELICATION NUMBER: 09/52,317
PRIOR PELICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: PL-FL_Genes Version 1.0
SEQ ID NO 105
LENGTH: 6222
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 105, Application US/10098841
Publication No. US20020197679A1
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                                                                                                                                                                                                                                                                                                                              347 ACGTACGCAGGAGAGCTGCTTTTG 370
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Best Local Similarity 54.6%;
Matches 77; Conservative (
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
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Chen, Rui-hong
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Zhao, Qing A.
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Wehrman, Tom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (707)..(3379)
US-10-098-841-105
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                                  Similarity
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US-10-098-841-105/c
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                                  Best Local Sir
Matches 121;
                  Query Match
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                       508 TAAACAAAAGGGGACTIGTIGAGAAGICCIGITITIATACCITGGAGCAAAACAITACAA 567
                                                                                                                                                                                                                                                                                                                                                                                                        85 TAAAATCCCTTGTAAATCTTTTAAAACTCTTTTAAAATCCCTTGTAAATCTATTTCCCGC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                           568 TGTAAAAATAAACAAAACCTGTTATTTTTTTTTTTTAAGAAGGTAATCGGGAGACGTAG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 CAAAAAAAAAAATTGGGGGAAAATATGTTTGAAAACAAATTTTGGCGGAAATTTAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489 GTATTTTTATAGACCTTTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTATATACC 548
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121-52701
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                  0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PILING DATE: 2001-06-22
SEO ID NO 3235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 342 LENGTH: 338
                                                                                                                                                                                                                                 Score 38;
                                                                                                                                                                                                                                                   Pred. No
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APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aljun
APPLICANT: Stolk, John A.
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Best Local Similarity 47.8%;
Matches 110; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: Homo sapiens US-10-046-935-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                            US-09-938-842A-3235
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                                                                                                                                                           TYPE: DNA
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Pred. No. 0.85;
0; Mismatches 69; Indels
                                                                                                     APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REPERBYCE: 210121.527
CURRENT APPLICATION UNDRER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed: January 17, 2003, 02:04:09
ne : 112 secs
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                      Sequence 342, Application US/09878178 Patent No. US20020177552A1
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Best Local Similarity 53.4
Matches 79; Conservative
                                                                GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapien
US-09-878-178-342/c
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Sequence 11, A
Sequence 29, A
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Sequence 8,
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TITLE OF INVENTION: RECLIPROCAL SUBTRACTION DIFFERENTIAL
TITLE OF INVENTION: DISPLAY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: COOPER & Dunham LLP
STRET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                         US-09-134-001C-135
US-08-184-009-119
US-08-458-356-119
US-08-460-736-119
                                                   US-09-004-838-93
US-08-213-419B-3
                                                                             US-07-924-028A-5
US-08-078-090-3
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US-08-544-332-8
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US-08-334-639-1
                                         JS-08-213-419B-1
                                                                                                                    US-08-232-463-14
                                                                                                                                                                                                   JS-09-461-474-11
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 55551/JPW/AMG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09032684 Patent No. 5882874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 177 base pairs
TYPE: nucleic acid
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Matches 157; Conservative
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RY: USA
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ZIP: 10036
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Sequence 19
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-385-982-376

US-08-117-083-23

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US-09-337-2068-6

US-09-337-2061-16

US-09-357-2061-16
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US-09-357-206A-21
US-09-357-206A-18
US-09-357-206A-20
US-09-357-206A-20
US-09-357-206A-20
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US-08-197-792-32
US-08-459-850-32
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US-08-257-073-2
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                                                                                                                                                                                                                                   441362 seqs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                          nucleic search, using sw model
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length: 2000000000
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378 TTCATGATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGT 437
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                                                                                                                                                                                                                                                                                                                                                                        258 ITGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAACTC 317
                                                                                                                                                                                                                                                                                                                 1021 TGAGCGTATGGCAAACGAAGGAAAATAGTTATAGTAGCCGCACTCGATGGGACATTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           901 AACTGCTGTGTATGAAATGCTTTAAG 874
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; OTHER INFORMATION: n = A,T,C or
US-09-385-982-376
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Best Local Similarity 62.69
Matches 107; Conservative
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ORGANISM: Homo sapiens
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US-09-385-982-376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 TGGTGGAGGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGT
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14.1%; Pred. No. 0.0066;
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CURRENT APPLICATION DATA:
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Best Local Similarity 14.1%; Pred. No. 0.0066;
Matches 80; Conservative 214; Mismatches 274;
                                                                                                                                                                   Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: BCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIL...
APPLICATION.
APPLICATION NUMBER: EP > FILING DATE:
FILING DATE: 26-A0G-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 109883-4109
"""AX: (703)683-4109
                                                   744 GAAAATATTATGTTTATGTAAAAAAAAAATCATGT 780
                                                                     121 GAAAATATTATGTTTATGTAATAAAAAAATCATGT 157
                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: '435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & La
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
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TOPOLOGY: lin
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                                                                                                                                                     US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 GTTTCNGGTAAACNGGAAT-ATAANGNGAAAGAACAAACNTTGGAACATACTTAATGGAT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITIATAGACCITIGIAAACAAAAGGGGACTIGT-----TGAGAAGICCIGITITIAIA 546
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Pred. No. 0.029;
0; Mismatches 54; Indels
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-01-87
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 376 LENGTH: 611
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GENERAL INFORMATION:
APPLICANT: Dinesh-Kumar, S.
APPLICANT: Datesh-Kumar, S.
APPLICANT: Baker, Barbara
APPLICANT: Baker, Barbara
APPLICANT: Baker, Barbara
APPLICANT: Baker, Barbara
BILE REFERENCE: 042250/191805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 60/093,494
PRIOR FILING DATE: 1998-07-20
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 ATTAATGTGGTTTGCAGATCTGGGGGTATCTGGTAAACTGGAATAATTAAGTTAAAGGAC 470
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                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CAURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILLIG DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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49.5%; Pred. No. 0.18;
tive 0; Mismatches 100;
  APPLICAN: ADDITION: Alan J. APPLICANT: Munro, Alan J. TITLE OF INVERTION: Recombinant Virus Vectors TITLE OF INVENTION: Papilloma Virus Proteins
                                                                                                                         ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09357206A Patent No. 6372962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
Inglis, Stephen C.
                                                                                                                                                                                                                                                                             Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 49.5 Matches 98; Conservative
                                                                              NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                 CITY: San Francisco
STATE: CA
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US-09-357-206A-6/c
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                                                                                                                                APPLICANT: Boursnell, Michael E.
APPLICANT: Inglis, Stephen C.
APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 720;
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Pred. No. 0.12;
0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                       Sequence 23, Application US/08117083 Patent No. 5719054 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/08117083
Patent No. 5719054
GENERAL INFORMATION:
APPLICANT: Boursnell, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFRENCE/DOCKET NUMBER: A-587
TELEPONUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEX: 415-398-3249
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 49.5%;
Matches 98; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 720 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: CDNA
US-08-117-083-23
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                                                 US-08-117-083-23
                                                                                                                                                                                                                                                                                                                                                          STATE: C. COUNTRY:
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SEQ ID NO 17
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                                                                                                                                                                                                                                                                                               TYPE: DNA
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Patent No. 6372952
GENERAL INFORMATION:
APPLICANT: Dinesh-Kumar, S.
APPLICANT: Baker, Barbara
TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs
FILE REPERENCE: 042250/191805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT FILING DATE: 1999-07-20
PRIOR PILING DATE: 1998-07-20
                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 IIGACAIIGIAIIGCIGCAAGAIIAAIGIGGIIIGCAGAICIGGGGGIAICIGGIAAACI 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 GGAATAATTA--AGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTATAGACCTTTG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          508 TAAACAAAAGGGGACTTGTTGAGAAGTCCTGGTTTTTATACCTTGGAGCAAAACATTACAA 567
                                                                                                                                                                                                  390 TIGACATIGIATIGCIGCAAGATTAATGIGGTTTGCAGATCTGGGGGTATCTGGTAAACT 449
                                                                                                                                                                                                                                                                        450 GGAATAATTA--AGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTTATAGACCTTTG 507
                                                                                                                                                                                                                                                                                                                                              508 TAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACATTACAA 567
                                                                                                                                                                                                                                                                                                          1430 TGGAAAATTACTTGTTAAGAAACTGAATAAAGGTAAATTATTATATTTATACTATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: CDNA-N/intron construct: E1-E2-E3-I3-E4-E5 US-09-357-206A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.7%; Score 37; DB 4; Length 5253; Best Local Similarity 50.7%; Pred. No. 0.64; Matches 115; Conservative 0; Mismatches 110; Indels
                                                                                                                            DB 4; Length 1818,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3158 TAGACGAAATTATATTTTAAGTTAATTTTCTAATATTTAGGATTTTA 3112
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1310 TAGACGAAATTATATTTTAAGTTAATTTTCTAATATTTAGGATTTTA 1264
                                                                                                                                                                                                                                                                                                                                                                                                                        568 IGTAAAAATAAACAAAACCIGITAIITITITITITITTAAGAAGGTAA 614
                                                                                                                                                                0; Mismatches 110;
                                                                                                                            Score 37;
                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 22
SOFFWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 5253
 PatentIn version 3.0
                                                                                                                          4.78;
                                                    TYPE: DNA
ORGANISM: Nicotiana glutinosa
                                                                                                                                            Best Local Similarity 50.79
Matches 115, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-357-206A-16/c
                                   1818
                                                                                     US-09-357-206A-6
SOFTWARE:
SEQ ID NO 6
LENGTH: 181
                                                                                                                            Query Match
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RESULT 8

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Sequence 17, Application US/09357206A
Sequence 17, Application US/09357206A
Sequence 17, Application US/09357206A
Sequence 17, Application US/09357206A
GENERAL INFORMATION:
APPLICANT: Dinesh Yumar, S.
APPLICANT: Dinesh Yumar, S.
TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs FILE REFERENCE: 042250/191805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT FILING DATE: 1999-07-20
PRIOR FILING DATE: 1998-07-20
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PRIOR FILING DATE: 1998-07-20
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PRIOR FILING DATE: 1998-07-20
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50.7%; Pred. No. 0.65;
1ive 0; Mismatches 110; Indels
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Patent No. 6372962
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SOFTWARE: PatentIn version 3.0
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Matches 115; Conservative
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Matches 115; Conserv
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US-09-357-206A-19
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Score 37; DB 4; Length 6095; Pred. No. 0.68; 0; Mismatches 110; Indels

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390 TTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGTATCTGGTAAACT 449
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                                                                            FEATURE:

COTHER INFORMATION: CDNA-N/intron construct: E1-E2-I2-E3-I3-E4-E5

US-09-357-206A-18
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Best Local Similarity 50.7%;
Matches 115; Conservative
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SOFTWARE: Patentin v
SEQ ID NO 20
LENGTH: 6325
                                                       ORGANISM: artificial
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SEQ ID NO 18
LENGTH: 6095
                                         TYPE: DNA
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12.09-357-206A-18/C
15 Sequence 18, Application US/09357206A
15 Patent No. 637296.
16 GENERAL INFORMATION:
17 APPLICANT: Dinesh-Kumar, S.
18 APPLICANT: Dinesh-Kumar, S.
18 APPLICANT: Daker, Barbara
18 TILLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs
19 TILLE OF INVENTION UNBER: US/09/357,206A
19 CURRENT APPLICATION NUMBER: US/09/357,206A
19 PRIOR FILING DATE: 1999-07-20
19 PRIOR FILING DATE: 1999-07-20
19 NUMBER OF SEQ ID NOS: 22
19 SOFTWANE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dinesh-Kumar, S.
APPLICANT: Baker, Barbara
APPLICANT: Baker, Barbara
TITLE COF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs
FILE REFERENCE: 042250/191805 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT FILING DATE: 1999-07-20
PRIOR PAPLICATION NUMBER: US 60/093,494
PRIOR FILING DATE: 1998-07-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
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                                3508 IGGAAAATTACTIGITAAGAAACIGAATAAAGGIAAATTATTATATTIATACTATATTA 3449
            450 GGAATAATTA--AGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTATAGACCTTTG 507
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; OTHER INFORMATION: cDNA-N/intron construct: E1-I1-E2-E3-I3-E4-I4-E5
US-09-357-206A-21
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Sequence 20, Application US/09357206A
Patent No. 6372952
GENERAL INFORMATION:
APPLICANT: Dinesh.Kumar, S.
APPLICANT: Baker, Barbara
TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs
FILE REPERENCE: 042250/191805 (5830-5)
CURRENT FILING DATE: 1999-07-20
PRIOR PPLICATION NUMBER: US 60/093,494
PRIOR FILING DATE: 1999-07-20
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4000 TAGACGAAATTATATTTTAAGTTAATTTTTCTAATATTTAGGATTTTA 3954
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Matches 115; Conservative
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US-08-261-663A-1
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                                   Sequence 22, Application US/09357206A
Patent No. 6372962
PAPLICANT: Dinesh Kumar, S.
APPLICANT: Baker, Barbara
TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs FILE REPERBNCE: 042290/19405 (5830-5)
CURRENT APPLICATION NUMBER: US/09/357,206A
CURRENT FILING DATE: 1999-07-20
PRIOR PILING DATE: 1998-07-20
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Patent No. 5571706
GENERAL INFORMATION:
APPLICANT: Baker, Barbara J
APPLICANT: Whitham, Steven A
TITLE OF INFUNION: Plant Virus Resistance Gene and Methods NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 4; Length 6428;
Pred. No. 0.7;
0; Mismatches 110; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,663A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Margaret A. Connor, USDA-ARS
STREET: 800 Buchanan Street
CITY: Albany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 0094.94
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
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Best Local Similarity 50.7%;
Matches 115; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Connor, Margaret A
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RESULT 13
US-09-357-206A-22/c
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SEQ ID NO 22
LENGTH: 6428
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4643 TGGAAAATTACTTGTTAAGAAACTGAATAAAGGTAAATTATTATATTTATACTATATA 4584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 GGAATAATTA--AGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTATAGACCTTTG 507
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APPLICANT: Baker, Barbara J
APPLICANT: Whitham, Steven A
AITLE OF INVENTION: Plant Virus Resistance Gene and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 1; Length 7400;
Pred. No. 0.75;
0; Mismatches 110; Indels
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TECT-1039-07754A-1/C

Sequence 1, Application PC/TUS9507754A

GENERAL INFORMATION:
                                                                                                                                                                                                                                               ORGANISM: Nicotiana glutinosa
TISSUE TYPE: leaf
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 559-6067
TELEFAX: (510) 559-577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7400 base pairs
                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 800 Buchanan Street
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Best Local Similarity 50.7%;
Matches 115; Conservative
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MEDIUM TYPE: Floppy disk
                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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6601..6933
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NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Margaret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
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390 TIGACATIGIATIGCIGCAAGATIAATGIGGITIGCAGATCIGGGGGTATCIGGIAAACT 449
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6934..6951)
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join(294..772, 1003..2098, 2941..3213, 5032..6600,
6934..6951)
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Pred. No. 0.75;
0; Mismatches 110; Indels
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                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07754A
                                                                                                                      ALTLICATION NUMBER: PCT/US95,
CLASSIFETATION:
ATTORNEY/AGENT INFORMATION:
NAME: CONDOT, MATGATEN A
REGISTRATION: NUMBER: 30043
REFERENCE/POCKET NUMBER: 30043
REPERENCE/POCKET NUMBER: 0094.
TELEPAN: (510) 559-6067:
TELEFAN: (100) 559-6067:
TELEFAN
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 50.7%;
Matches 115; Conservative
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PCT-US95-07754A-1
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NAME/KEY:
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Search completed: January 17, 2003, 02:02:32 Job time : 100 secs Page

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Rat Progression Su
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                                                                                                                                            January 16, 2003, 21:51:23 ; Search time 143 Seconds (without alignments) 75.478 Million cell updates/sec
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1 MNVEHEVNLLVEEIHRLGSK.....AGELLLQGVHDDVDIVLLQD 81
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAU76533
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Novel human diagno Drosophila melanog H. pylori HPCO24 p Human cytoskeleton Novel human protei Human MDDT SEQ ID Herbicidally activ Propionibacterium Herbicidally activ Horbicidally activ Horbicidally activ Horbicidally activ Horbicidally activ Herbicidally activ Herbicidally activ Horbicidally activ Horbicidally activ Horbicidally activ Horbicidally activ Herbicidally activ Horbicidally activ Herbicidally activ	Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Myosin heavy chain Arabidopsis thalia	n 13). en 13; cytostatic; cancer; oid tumour; leukaemia; colon.	Gene 13 for preventing the vessels, and for treating
ABG27995 ABB58876 ABB60049 AAB46383 AAX91948 ABB97460 ABP51430 ABB92013 ABB92013 AAW98798 AAW71554		81 AA. Gene 13 (rPSGen 1 Gene 13; rPSGen 1 1 tumour; thyroic	K. Suppressed new blood
11.1856 22.28.29.29.29.29.29.29.29.29.29.29.29.29.29.	9 387 9 398 9 398 9 398 9 398 9 573 9 573 9 1113 1305 1314 157 157	dard; Protein; 8 (first entry) lon Suppressed Ge sion Suppressed G	WO-US2679 US-064833 MBIA NEW D, Su Z, 32.
106 106 106 107 108 108 108 108 108 108 108 108	41 (5.00) 40 (5.00)	32 AU76532 star AU76532; 5-JUN-2002 at Progress: 1004 vessel.	
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Human secreted pro Arabidopsis thalia Arabidopsis thalia PSGen13 protein.

Human nervous syst

AAY39325 ABB14740 AAG58354 AAG58353 AAB32055

87 83 95 161 92

Human prostate can Human secreted pro

AAB56907 AAG58854

Human Progression

Zea mays protein f

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12-MAR-1999;
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                                                     rat or human progression Suppressed Gene 13 (PSGen 13) protein. The nucleic acids are useful for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer, e.g. nasopharyngeal tumour, thyroid tumour, leukaemia, lymphoma, or cancer of the breast, lung, prostate, ovary or colon. PSGen 13 may also he used to suppress the transformed phenotype of a malignant cell. Administration of PSGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour marker, tumour mass, number of partient serum tumour marker, tumour improved clinical symptoms, and/or increased patient survival. The present sequence represents the amino acid sequence of rat Progression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel isolated nucleic acids which encode a rat or human Progression Suppressed Gene 13 (PSGen 13) protein. The nucleic acids are useful for preventing the growth of cancer cells and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, Progression Suppressed Gene 13; rPSGen 13; cytostatic; cancer; blood vessel; nasopharyngeal tumour; thyroid tumour; leukaemia; lymphoma; breast; lung; prostate; ovary; colon.
                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                       1 MNVEHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVT 60
                                                                                                                                                                                                                                                                                       invention relates to novel isolated nucleic acids which encode a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing the for treating
                                                                                                                                                                                                                               Length 81;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New rat and human Progression Suppressed Gene 13 for growth of cancer cells and/or new blood vessels, and
                                                                                                                                                                                                                           100.0%; Score 406; DB 23;
100.0%; Pred. No. 5.9e-46;
Live 0; Mismatches 0;
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patients suffering from a cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patients suffering from a cancer
                                                                                                                                                                                 Suppressed Gene 13 (rPSGen 13).
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                      Claim 28; Fig 1; 53pp; English.
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Matches 81; Conserv
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new blood vessels, and for treating patients suffering from a cancer, e.g. nasopharyngeal tumour, thyroid tumour, leukaemia, lymphoma, or cancer of the breast, lung, prostate, ovary or colon. PsGen 13 may also be used to suppress the transformed phenotype of a malignant cell. Administration of PsGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour marker, tumour metastasis, vascularisation, perfusion, or rate of tumour growth, improved clinical symptoms, and/or increased patient survival. The present sequence represents the maino acid sequence of human Progression Suppressed Gene 13 (HupsGen 13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNVEHEVNILLYEEIHRIGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF15566 to AAF16505 encode the human prostate cancer associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 390; DB 23;
Pred. No. 7.7e-44;
4; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB56907 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.1%;
93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.8
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   81 AA;
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polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the isolation of genes AAC66410-C66458 encoding the human secreted proteins AAB32002-B32050. This sequence represents a fragment of the protein encoded by the gene given in the descriptor line. The sequence is used as a query sequence for doing BLASTX searches to determine homologous sequence to the protein. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                              1 MNVEHEVNILVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                        Score 390; DB 21; Length 142; Pred. No. 1.6e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein BLAST search protein SEQ ID NO: 114.
                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecules encoding human secreted proteins,
                                                                                                                                                                                                                                            4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB32056 standard; Protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                          122 YPGELLLQGVHDDVDIILLQD 142
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                                                                                                                                                                                                      96.1%;
93.8%;
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99US-0171552.
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                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                    142 AA;
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22-DEC-1999;
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                                                                                                                                                                                                                                        16;
                                                                                                                               invention.
                                                                                                                                                                     Sequence
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and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, luiver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) eardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                              1 MNVEHEVNILVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVT 60
                                                                                                                                                                                                                           6 MNVDHEVNLLVEEIHRLGSKNADGKLSVKFGVLFRDDKCANLFEALVGTLKAAKRKIVT 65
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                                                                                                                                                            Length 83;
                                                                                                                                                                                       1; Indels
                                                                                                                                                          Score 375; DB 21;
Pred. No. 7.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays protein fragment SEQ ID NO: 76054.
                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                          AAG58854 standard; Protein; 87 AA.
                                                                                                                                                          92.48;
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                                                                                                                                                                                                                                                                              66 YPGELLLQGVHDDVDIIL 83
                                                                                                                                                                                                                                                                  61 YAGELLLQGVHDDVDIVL 78
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                                                                                                                                                         Query Match
Best Local Similarity 93.6
Matches 73; Conservative
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                                                                                                                                   83 AA;
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                                                                                                         infections.
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                                                                                                                                   Sequence
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990S-0145918. 990S-0145919. 990S-0146386. 990S-0146388. 990S-0146388. 990S-0147038. 990S-014704. 990S-0147192. 990S-0147192. 990S-0147192.	990S-01474935. 990S-0147935. 990S-01481791. 990S-0148341. 990S-0148368. 990S-0149368. 990S-0149475. 990S-0149725. 990S-0149725. 990S-0149729. 990S-0149729. 990S-0149729. 990S-0149930. 990S-0149930. 990S-0150884.	990S-01519438 990S-0151930 990S-0152363 990S-0153070 990S-0154039 990S-0154039 990S-0155139 990S-0155139 990S-0155659 990S-0155659 990S-0156596 990S-0156596	9905-0158232 9905-0158232 9905-0159295 9905-0159295 9905-0159330 9905-0159331 9905-0159331 9905-0159637 9905-0159637 9905-0160741 9905-016076 9905-016076 9905-0160981 9905-0160981 9905-0160981 9905-0160981 9905-0160981
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99US-0134370. 99US-0134768. 99US-0134941. 99US-0135124. 99US-0135523. 99US-0135629. 99US-0136021. 99US-0136782. 99US-0136782. 99US-0136782. 99US-0137722.	99US-0138094 99US-0138647 99US-0138447 99US-0139452 99US-0139453 99US-0139454 99US-0139456 99US-0139456 99US-0139456 99US-0139456 99US-0139460 99US-0139462 99US-0139462 99US-0139462 99US-0139462 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463	990S - 0140354 990S - 0140695 990S - 0140695 990S - 0141287 990S - 0141287 990S - 014265 990S - 014265 990S - 014263 990S - 0142803 990S - 0142803 990S - 014324 990S - 014324 990S - 014324 990S - 0143624 990S - 0143624	990S - 0144086 990S - 0144335 990S - 0144333 990S - 0144333 990S - 0144334 990S - 0144335 990S - 0144352 990S - 0144864 990S - 0144864 990S - 0145086 990S - 0145086 990S - 0145087 990S - 0145087
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99US-0134941
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                                                                                                                                                                                                                                                                                                                18-OCT-2000 (first entry)
                                                                                                                        55; Conservative
                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                             Best Local Similarity
                                                                             83 AA;
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    allergies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the isolation of genes AAC66410-C66458 encoding the human secreted proteins AAB32002-B32050. This sequence represents a peptide fragment homologous to the protein encoded by the gene given in the descriptor line. The sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, amedical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease,
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                                                                                                                        Gaps
                                                                                                                                           1 MNVEHEVNLLVEETHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVT 60
                                                                                                                                                        Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers
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                                                                                                 Length 87;
                                                                                                                                                                                                                                                                                                                                    Human secreted protein BLAST search protein SEQ ID NO: 113
                                                                                                                       Indels
                                                                                                                         13;
                                                                                               Score 302; DB 21;
Pred. No. 3.7e-32;
7; Mismatches 13;
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                                                                                                                                                                                                                                                                  AAB32055 standard; Protein; 83 AA.
                                                                                                  74.48;
74.78;
        990S-0161359.
990S-0161360.
990S-0161361.
990S-0161920.
990S-0161993.
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                                                                                                                                                                                                   61 YEGELLLQGVHDNVEITLL 79
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 99US-0161406
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                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-602357/57.
                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                              26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
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          26-0CT-1999
26-0CT-1999
                                                               28-OCT-1999
29-OCT-1999
                                                                                                            Best Local Sim
Matches 59;
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0-MAY-1999 11-MAY-1999 4-MAY-1999 5-MAY-1999 7-MAY-1999 1-UUN-1999 4-UUN-1999 6-UUN-1999 0-UUN-1999	16-JUN-1999; 17-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 23-JUN-1999; 23-JUN-1999; 23-JUN-1999; 23-JUN-1999; 24-JUN-1999; 24-JUN-1999; 25-JUN-1999; 01-JUL-1999; 01-JUL-1999; 06-JUL-1999; 112-JUL-1999; 113-JUL-1999; 113-JUL-1999; 113-JUL-1999; 113-JUL-1999; 113-JUL-1999; 113-JUL-1999; 113-JUL-1999; 113-JUL-1999;	6. JUL - 1999 9. JUL - 1999 10. JUL - 1999 11. JUL - 1999 12. JUL - 1999 13. JUL - 1999 14. JUL - 1999 15. JUL - 1999 16. JUL - 1999 17. JUL - 1999 18. JUL - 1999 19.
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AUG-1999 AUG-1999 AUG-1999 AUG-1999 AUG-1999 AUG-1999 AUG-1999 AUG-1999 AUG-1999 AUG-1999	3 - AUG-199 6 - AUG-199 8 - AUG-199 0 - AUG-199 0 - AUG-199 0 - AUG-199 3 - AUG-199 5 - AUG-199 7 - AUG-199 7 - AUG-199	1. AUG 1999 1. SEP 1999 0. SEP 1999 0. SEP 1999 6. SEP 1999 6. SEP 1999 1. SEP 1999	20-001-1999 7-001-1999 8-001-1999 8-001-1999 3-001-1999 3-001-1999 4-001-1999 4-001-1999 4-001-1999	1-0CT-1999 1-0CT-
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99US-014432.
99US-0144632.
99US-0144814.
99US-0145086.
99US-0145088.
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990S-0139750.
990S-0139763.
990S-0139817.
990S-0139899.
990S-0140353.
990S-0140353.
990S-0140354.
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99US-0144086.
99US-0144325.
99US-0144331.
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99US-0145089.
99US-0145192.
          990S-0136392,
990S-0136782,
990S-0137222,
990S-0137528.
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99US-0139457.
99US-0139458.
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99US-0139461.
99US-0139462.
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99US-0139492.
99US-0139454.
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                                                                                                                                                                                   99US-0139459
                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                             0; Gaps
                                                        Query Match 70.4%; Score 286; DB 21; Length 95; Best Local Similarity 70.5%; Pred. No. 5.5e-30; Matches 55; Conservative 8; Mismatches 15; Indels
                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 75316.
                                                                                                                                                                                                   AAG58353 standard; Protein; 161 AA
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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990S-0123180.
990S-0123548.
990S-0126788.
990S-0126644.
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99US-0135353.
99US-0135629.
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99US-0128714.
99US-0129845.
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99US-0132407
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                                                                                                                                  61 YAGELLLQGVHDDVDIVL 78
                                                                                                                                            18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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28-APR-1999;
28-APR-1999;
30-APR-1999;
04-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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25-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
110-APR-1999;
21-APR-1999;
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14-MAY-1999;
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99US-0161993.

28-OCT-1999; 29-OCT-1999;

PR PR

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PR 04-NGC-1999; 990S-0147038.

PR 04-NGC-1999; 990S-0147038.

PR 06-NGC-1999; 990S-0147320.

PR 06-NGC-1999; 990S-0147320.

PR 06-NGC-1999; 990S-0147320.

PR 11-NGC-1999; 990S-0147416.

PR 20-NGC-1999; 990S-0147416.

PR 20-NGC-1999; 990S-0147416.

PR 20-NGC-1999; 990S-014972.

PR 20-NGC-1999; 990S-014976.

PR 20-NGC-1999; 990S-014976.

PR 21-NGC-1999; 990S-014976.

PR 21-NGC-1999; 990S-0149772.

PR 21-NGC-1999; 990S-0149772.

PR 21-NGC-1999; 990S-015100S.

PR 21-NGC-1999; 990S-01510S.

PR 21-NGC-1999; 990S-015978.

PR 21-NGC-1999;
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This is the amino acid sequence of the PSGen13 protein (progression suppressed gene 13). PSGen13 has suppressed expression in progressed tumour cells. The PSGen13 nucleic acids sequence was identified using new tethods for identifying nucleic acids differentially expressed between two samples. The method involves performing reciprocal subtraction two samples. The method involves performing reciprocal subtraction samples. The subtraction samples are amplified and compared to identify those nucleic acids that are differentially expressed. The subtraction samples are amplified and compared to identify those with increased or reduced expression during tumour cell progression, e.g. progression suppressed genes (PSGen) and cell progression e.g. progression alterated genes (PSGen). The method reduces the complexity of the band pattern produced in conventional differential RNA display (where bands may be obscured, resulting in false positive signals) since most bands common to both samples are eliminated, allowing identification and coloning of genes displaying anticipated differential expression. RSDD requires only a single anchored primer for amplification and reamplified conn be analysed by reverse Northern blotting.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying nucleic acids differentially expressed between two samples, particularly sequences involved in tumour progression
                                                                                                                                                                                                                                                                                                                                                                                                Progression suppressed gene; PSGen; progression elevated gene; PEGen; tumour; reciprocal subtraction differential RNA display; RSDD; differential expression; gene cloning; cancer.
                                                                                        Gaps
                                                                 1 MNVEHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVT 60
                                       ö
     Length 161;
                                     Indels
                                       15;
70.4%; Score 286; DB 21; 70.5%; Pred. No. 1.1e-29; iive 8; Mismatches 15;
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                                                                                                                                                                                                                                                          AAY39325 standard; Protein; 92 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0197889.
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                                                                                                                                       61 YAGELLLQGVHDDVDIVL 78
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                                     Conservative
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N-PSDB; AAZ21517.
              Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                PSGen13 protein.
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 Query Match
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2000US-0231414.
2000US-0232080.
2000US-0232081.
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13-0CT-2000)
20-0CT-2000)
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14-SEP-2000;
14-SEP-2000;
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                                                                                                                                                                                                                                                                           Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; imunosoppressive; antihiflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiatrhitic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antialheepic; antiidiabelic; antiulcer; anticonvulsant; antihingal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                            Gaps
                                                               Length 92;
                                           Indels
                                                                                                                                                                                                                                                        Human nervous system related polypeptide SEQ ID NO 3397.
                    Query Match 57.1%; Score 232; DB 20; Best Local Similarity 72.7%; Pred. No. 7.4e-23; Matches 48; Conservative 4; Mismatches 8;
                                                                                                                                                                                     ABB14740 standard; Protein; 77 AA.
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2000US-0205515.
2000US-0209467.
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2000US-0224518.
2000US-0224519.
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2000US-0215135
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92 AA;
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                                                                                                          YAGELL 66
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24 - FEB - 2000;
02 - MAR - 2000;
17 - MAR - 2000;
18 - APR - 2000;
19 - MAY - 2000;
07 - JUN - 2000;
30 - JUN - 2000;
07 - JUL - 2000;
07 - JUL - 2000;
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26-JUL-2000;
26-JUL-2000;
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I-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
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Sequence
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Novel human diagnostic protein #27986.

18-FEB-2002 (first entry)

ABG27995;

ABG27995 standard; Protein; 456 AA.

RESULT 11 ABG27995

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroditis, diabetes mellitus, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 3397; 1701pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                         2000US-0249214,
                                                                        2000US-0249213
                                                                                                                                                     2000US-0249218
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2000US-0249264
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2000US-0249299
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cancers and metastases
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Best Local Similarity
Matches 31; Conserv
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17-NOV-2000;
17-NOV-2000;
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31-DEC-2000;
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05-DEC-2000;
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06-DEC-2000;
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

biodiversity

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73.

N-PSDB; AAS92182

(HYSE-) HYSEQ INC.

30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217 23-AUG-2000; 2000US-0649167

WO200175067-A2. Homo sapiens.

11-OCT-2001

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colyperase chair reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The coloridates are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques of restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as (II). (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. (I polypeptide and polynucleotide sequences have applications in classocial subspectives. Abg00010-Abg30377 represent of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and conding and ordisequences as abg00010-Abg30377 represent novel human cut sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO contribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 26.1%; Score 106; DB 22; Length 456; Local Similarity 43.1%; Pred. No. 2.8e-05; nes 25; Conservative 10; Mismatches 21; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 58354; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456 AA;
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MNVEHEVNLLVEEIHRLGSKNADGKLSVKFGV 32

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Conservative

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention i useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176 ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microbial infection; antibacterial; Helicobacter pylori infection;
                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 6939; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 73; DB 22
Pred. No: 0.54;
9; Mismatches
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                                                                           Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 AA;
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                                     pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention is insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL015176-ABL30511), expressed DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.1%; Score 81.5; DB 22; Length 31.6%; Pred. No. 0.015; Ive 16; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 6939.
                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 3420.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB60049 standard; Protein; 399 AA.
                                   ABB58876 standard; Protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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Best Local Similarity 31.6 Matches 24; Conservative
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                                                                         ABB58876;
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RESULT 12
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Modified-site
    This invention describes a novel preparation of an agent (A) for detection, prevention and/or treatment of microbial infection by:

(d) identifying essential genes (I) and corresponding polypeptides

(II); (ii) identifying compounds that are directed against (II) and inactivate the microbe; (iii) testing these for suitability for use; and care directed against (II) and inactivate the microbe; (iii) testing these for suitability for use; and care of gene-deficient microorganisms by conditional antisense inhibition (CAI) and/or subtractive recombination mutagenesis (SRM).

The products of the invention have antibacterial activity. (A) (which may be a nucleic acid (Ia), vector or host cell containing (Ia), derived be a nucleic acid (Ia), vector or host cell containing (Ia), derived compared or inhibitor of (IIa) are particularly used for diagnosis, creatment or prevention of infection by Helicobacter pylori. Particularly contained or prevention of infection by Helicobacter pylori. Particularly contenting species, so identified (Ia) should have a broad spectrum of activity. Many gene-deficient cells can be screened quickly, in an automated process, and the identified genes can be used for screening without purification.
                                                                                                                        Preparing an agent for diagnosis or control of microbial infection, useful particularly against Helicobacter, based on identification of essential genes in defective mutants -
                                                                     Meyer TF;
                                 (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                    Hueck CJ,
                                                                                                                                                                     Claim 37; Figure 15; 366pp; German.
                                                                  Gibbs CP,
99DE-1027740.
                                            (CREA-) CREATOGEN GMBH.
                                                                 Apfel H, Fuchs TM,
                                                                                       WPI; 2001-049948/06.
N-PSDB; AAF25660.
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17-JUN-1999;
21-JUL-1999;
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ä Gaps 3, Length 116; 24 GKLSVKFGVLFQDDRCANLFEAL-VGTLKAAKRRIVTYAGELLLQGVHD 72 26 GGLFIGFVKVWQKDVLAQLMEHLETGQYK--KREKTLAYMTKLLEQGIHE 73 Indels 21; Score 66.5; DB 22; Pred. No. 0.8; 6; Mismatches 16.4%; Best Local Similarity 40.0 Matches 20; Conservative Query Match g ð

Cytoskeleton associated protein; CYSKP-3; cancer; proliferative; autoimmunity; inflammatory, vesicle trafficking; neurological; cardiovascular; cell motility; reproductive; muscle disorder. Human cytoskeleton associated protein 3 (CYSKP-3). "ankyrin repeat" Location/Qualiflers AAY91948 standard; Protein; 324 19-JUL-2000 (first entry) 'note= Homo sapiens AAY91948; Domain RESULT 15 AAY91948 ID AAY9

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AAY91946-61 show human cytoskeleton associated proteins 1 to 16 (CYSKP-16 CYSKP-16) respectively. The sequences can be used to treat and diagnose cancer and cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cardiovascular, cell motility, reproductive and muscle disorders. Pharmaceutical compositions containing CYSKP-2 to CYSKP-16 can be used to treat or prevent disorders associated with decreased expression or activity of CYSKP (claimed), for example, atherosclerosis, cirrhosis, hepatitis, myelofibrosis, psoriasis, cancers, autoimmune/antinflammatory disorders such as allergies, anemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytoskeleton associated proteins, used to treat cell proliferative, autoimmune/inflammatory, vesicle trafficking, neurological, cell motility, reproductive and muscle disorders
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"potential phosphorylation site"
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Baughn MR;
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Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "potential
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99US-0131321
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304
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27-APR-1999;
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Ř 324 Sequence

(claimed).

"potential phosphorylation site"

/note= 76..85

Domain

/note-

"ankyrin repeat"

"ankyrin repeat"

'note=

Modified-site

Domain

asthma, acquired immunodeficiency syndrome (AIDS), Crohn's disease, diabetes mellitus, Goodpasture's syndrome, osteoarthritis, scleroderma and trauma. CYSKP antagonists can be used to treat or prevent a disorder associated with increased expression or activity of CYSKP

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Ouery Match
Best Local Similarity 29.2%; Pred. No. 4.7;
Matches 21; Conservative 11; Mismatches 30; Indels 10; Gaps
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Search completed: January 17, 2003, 02:06:36 Job time : 144 secs

Q8ztyl pyrobaculum Q9wzm8 thermotoga Q9xz44 lutzomyla 1 Q9zq96 arabidopsis Q21458 caenorhabdi

O9WZM8

09X244

acinetobact

Q9sz40 arabidopsis

Q92Q96 Q21458 Q9S240 Q9ZQ99 Q9ZQ98 Q98ZQ98 Q9SZQ98 Q9ZQ98 Q9ZQ9ZQ

Q8YKJ4 Q8R841

Q9GV11 O96069 O96068

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            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:* sp_bacteriap:* sp_organelle:* sp_phage:* sp_archeap:* sp_rodent: * sp_rvirus:* sp_plant:* sp_virus:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	יין וייספורה פווש פוואססס	Ogolf3 homo sanien	Ognoal homo sanien	O81881 arabidonsis	O62234 caenorhabdi	O46052 drosophila	Ogvzw6 drosophila	022133 caenorhabdi	085431 rice strine	O98ax3 mycoplasma	Ogopi4 campylobact	OBsto6 encephalito	Ogsrm7 arabidonsis	093w32 arabidonsis	O9sn36 arabidonsis	Ognahy homo sanien
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	Query Match Length DB ID	81	81	141	161	162	371	183	289	2919	318	395	294	447	462	530	307
æ	Query Match	99.3	96.1	96.1	70.4	23.8	20.3	20.1	20.1	17.5	17.0	16.9	16.6	16.6	16.6	16.3	16.0
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Q8UGQ4 Q8XEW7 Q9JVG1 Q9CMX9 Q19056 Q8QZ10

RR 113

REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE TROUN-C57BL/63; TISSUE-EMBRYONIC HEAD;

RA MEDINE-21085660; DubMed-11217851;

RA Azawa T., Hara A., Shipheta K., Yoshino M., Itoh M., Ishii Y.,

RA Azawa T., Tazwa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Saito T., Okazaki Y., Gojobori T., Bonoo H., Kasukawa T., Saito R.,

RA Fistohmann W., Gasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,

Rotrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Rustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Rustincich S., Hill D., Mashima J., Mazzarelli J., Mombaerts P.,

Rotrone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,

Rasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Rasaki H., Sato K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Rasaki H., Rasaki Y.;

Rasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Rasaki H., Sato K., Voshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Rasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Rasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Rasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Rasaki H., Sato K., Wang K.H., Weitz C., Whittaki S.,

Rasaki H., Sato K., Wang K.H., Weitz C., Whittaki S.,

Rasaki H., Sato K., Wang K.H., Weitz C., Whittaki S., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK013984; BAB29100.1; -MGD; MGI:1920362; 3110003A17Rik. 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 3110003A17R1k protein. PRT; PRELIMINARY; Mus musculus (Mouse). NCBI_TaxID=10090; 3110003A17RIK. D9CXU3 RESULT 1 Q9CXU3

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Gaps

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Matches

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09P1F3

RESULT 2 Q9P1F3

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SEQUENCE FROM N.A.
Obermaler B., Deutschenbaur S., Piravandi E., Hoheisel J., Jesse T.,
Heijnen L., Vos P., Mewes H.M., Mayer K.F.X., Schueller C., Bevan M.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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 Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L., Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.; "Human partial CDS from cd34+ stem cells."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF161398; AAF2958.1; -.. NON_TER 1 1 SEQUENCE 141 AA; 15797 MW; 7FD16DF8BC359EFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Obermaier B., Deutschenbaur S., Piravandi E., Mewes H.W., Lemcke Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.4%; Score 286; DB 10; Length 161; larity 70.5%; Pred. No. 1.2e-25; Conservative 8; Mismatches 15; Indels
                                                                                                                                                          Length 141;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL031394; CAA20577.1; -
EMBL; AL161583; CAB80081.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 161 AA; 18337 MW; 4F42A35D064DE8B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
01-CCT-2100 (TrEMBLrel. 15, Last annotation update)
01-NOV-131 OR A
                                                                                                                                                   Ouery Match 96.1%; Score 390; DB 4; Le Best Local Similarity 93.8%; Pred. No. 6.4e-38; Matches 76; Conservative 4; Mismatches 1;
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Last sequence update)
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NCBL_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                  Score 403; DB 11; Length 81;
Pred. No. 9.4e-40;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BLOOD;
Strausberg R.;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF116683; AAF71102.1; -.
EMBL; BC014953; AAH14953.1; -.
Hypothetical protein.
SEQUENCE 81 AA; 9056 MW; IFODCE7AlD22B171 CRC64;
 9058 MW; B444C508ACE602C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PR02013 (Hypothetical 9.1 kDa protein)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
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Pred. No. 3.1e-38;
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93.8%;
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Best Local Similarity 93.8
Matches 76; Conservative
                                                                       Conservative
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SEQUENCE FROM N.A.
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81
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SEQUENCE
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RESULT 3

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STRAIN-BERKELEY
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CG2113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              optera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                    2 NVEHEVNLLVEEIHRLGSKNADG-KLSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVT 60
                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'From sequence to chromosome: the tip of the X chromosome of
                                                                                                                                                                                                                                                                   Query Match 23.8%; Score 96.5; DB 5; Length 162; Best Local Similarity 32.9%; Pred. No. 0.002; Matches 26; Conservative 16; Mismatches 34; Indels
                                                                                                                                                                                        Genome sequence of the nematode C.elegans: A platform for
                                                                                                                Cottage A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                            C21116625BBF64B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-00N-1998 (TrEMBLrel. 06, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) F36F2.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EG:152A3.3 protein (HL01173P).
EG:152A3.3 OR CG3630.
Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                  MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                    investigatíng biology.";
Science 282:2012-2018(1998).
EMBL; 281532; CABC4325.1; -.
SEQUENCE 162 AA; 18490 MW;
                                                                                                                                                                                                                                                                                                                                                                                     Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                      61 YAGELLLQGVHDDVDIVLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                   Caenorhabditis elegans.
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Ephydroidea; Drosophi
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                                                                                                  SEQUENCE FROM N.A.
                                                                          NCBI_TaxID=6239;
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Rabid J.F., Aphayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Rallew R.M., Basca A., Baxendala J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basca A., Baxendala J., Bayraktaroglu L., Beasley E.M., Rallew R.W., Basca A., Barenan B.P., Bhandari D., Bolshakov S., M., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Cadieu E., Center A., Chandra I., Raller R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Ra Burlis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Ra Poblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Ra Poblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Ra Borbin K.J., Evangelista C.C., Ferriaz C., Ferriaz C., Ferriaz S., Fleischmann W., RA Harris K.J., Evangelista C.C., Ferriaz C., Ferriaz S., Fleischmann W., Roslen D., Houston K.A., Heiman T.J., Hernandez J., Harris M., Harris M., Harris M., Harris M., Harris M., Harris M., Hostin D., Houston K.A., Heiman T.J., Hernandez J.Y., Ketchum K.A., Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Katchum C., Alalish P., Karpen G.H., Ke Z., Kennison J.A., Kasher B., Murphy B., Murphy L., Murphy E., Sollard J., Phiri W., Spardling A.C., Slander K., Scheeler F., Shen H., Shie B.C., Sladell Klamco G.S., Pan S., Pollard J., Phiras B., Spradling A.C., Stander E., Spradling A.C., Stander J., Woodage T., Woodag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Indels 15;
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SEQUENCE 371 AA; 39430 MW; 3C3B6D2E58FEB36D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
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Rhabditidae; Peloderinae; Caenorhabditis

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                                                                   RC STRAIN—EBERKELEY.
REALINE—20196066; Pubbed—10731132;
RADINE—20196066; Pubbed—10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., Butcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Britcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Britcon G.G., Mortman J.R., Paleson C.R., Miklos G.L.G., Randon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., Ra Beson K.Y., Basud A., Baxendala J., Baytaktarolu L., Beasley E.M., Ballew R.M., Basud M.R., Baurtis R.G., Helt G., Wolsketh D., Britchter P., Bottchan M.R., Boutch J., Brandari D., Bolshakov S., Bortchan M.R., Boutch J., Butler H.D., Bhandari D., Bolshakov S., Bortchan M.R., Buutler H.D., Bhandari D., Bolshakov S., Bottchan M.R., Dablike C., Davenport L.B., Davies P., Achen B.D., Butler R., Dougles E., Doucher A., Cadle E., Dourn P., Brits R.A., Cawley S., Dahlke C., Davenport L.B., Davies P., Butler R., Douglist C.C., Perraz C., Ferriac C., Ferriac C., Perraz C., Perra C., Perra C., Cabrich B.D., Butler R., Douglist C., Gabrieliata A.E., Oward D., Lais S., Dunkov B.C., Dunn P., Hostin D., Houston K.A., Haward T.J., Hernandez J.R., Harris M., Alush F., Karpen G.L., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li X., Minnel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li X., Minnel B.E., Rodira C.D., Morbirs J., Moosheri A., Moy M., Murphy B., Morphy D., Nusskern D.R., Melson D.R., Molson R.A., Nixon R., Nusskern D.R., Perce B., Speading A.C., Staphero M., Strong R., She R., Reinert K., Remington K., Saunders R., Wang S., Yao O.A., Sheng L., Randson D.R., Woodage T., Worley K.C., Wu D., Yang G., Zhu X., Smith H.O., Kaiben R., Tectro C., Thurer R., Wolley W., Wolley S., Zhan M., Zhong R., Williams S.M., Woodage T., Worley C., Chang S., Zhan R., Schence S. Britskas R., Feeter S., Speading A.C.,
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVNLLVEEIHRLGSKN-ADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRKIVTYAGE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 31.6'
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 287:2185-2195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-95088603; PubMed=7996149;

Toriyama S., Takahashi M., Sano Y., Shimizu T.;

Toriyama S., Takahashi M., Sano Y., Shimizu T.;

"Nucleotide sequence of RNA 1, the largest genomic segment of rice stripe virus, the prototype of the tenuivirus.";

J. Gen. Virol. 75:3569-3579(1994).

EMB.; D31879; BAR06139; Abd.short.

InterPro; IPR003323; OTU.
                                                                                                                                                                                                                                                                                                                                                                                                         26; Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                 Length 289;
                                                                                                                                                                                                             'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2919 AA; 336872 MW; 16FB7BC57FB12FC0 CRC64;
                                                                                        Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    investigating biology.";
Science 282:2018(1988).
EMBL: 235663; CAA84722.1; -
SEQUENCE 289 AA: 32972 MW; 20DB67F731F03098 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice stripe virus (isolate T) (RSV).
Viruses; ssRNA negative-strand viruses; Tenuivirus.
NCBI_TaxID=36394;
                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                            Query Match 20.1%; Score 81.5; DB Best Local Similarity 33.7%; Pred. No. 0.23; Matches 29; Conservative 14; Mismatches.
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PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
PROSITE; PS50802; OTU; 1.
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111 RKYGLVHFEGEMLYQRQDDEKIITML 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 KRRKIVTYAGELLLQGVHDDVDIVLL 79
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                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                           SEQUENCE FROM N.A.
NCBI_TaxID=6239;
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Q85431;
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Q98QX3;
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Q85431
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Length 395;

DB 16;

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Query Match 16.95
Best Local Similarity 26.25
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope;
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MEDLINE-2012; PubMed-10688204;
MEDLINE-2012; PubMed-10688204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouail M.A., Rajandraam M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                      Chambaud I., Hellig R., Ferris S., Barbe V., Samson D., Galisson F., Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C., Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 EVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDR-----CANLFE-----ALVGTLKAAK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
ou-ocT-2001 (TrEMBLrel. 18, Created)
01-oCT-2001 (TrEMBLrel. 18, Last sequence update)
01-oCT-2001 (TrEMBLrel. 18, Last annotation update)
Phosphate acetyltransferase (Phosphotransacetylase) (EC 2.3.1.8).
MYPU_2370.
                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Wucleic Acids Res. 29:2145-2153(2001).
BNBL; AL445563; ACA:3410.1; -.
Mypuilst; MYPU_2370; -.
InterPro; IPR002505; PTA_PTB.
Pfam; PF01515; PTA_PTB; 1.
                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.0%; Score 69; DB 16; Length 318; 36.2%; Pred. No. 7.7; 1ve 6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Acyltransferase; Complete proteome.
SEQUENCE 318 AA; 35015 MW; ECE864ClAAB7E3EF CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative integral membrane zinc-metalloprotease.
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InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF01435; Peptidase_M48; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                              MEDLINE-21267165; PubMed-11353084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Nature 403:665-668(2000).
EMBL; AL139076; CAB72997.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                       Mycoplasma pulmonis.
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Matches 29; Conserv
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE 395 AA;
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                                                                                                                                                                                                              NCBI_TaxID-2107;
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09PPI4
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                                                                                                            Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                            Gaps
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                                                                                  2 NVEHEVNLLVEE-----IHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=GB-MI;
MEDIINE=21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
Weissenbach J., Vivares C.P.;
                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence and gene compaction of the eukaryote parasite Encephalitozono cuniculi."; Nature 414:450-453(2001).
EMBL; ALS90451; CAD27101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.6%; Score 67.5; DB 5; Length 294; 29.9%; Pred. No. 10;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Encephalitozoon cuniculi.
Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon
NCBL_TaxID=6035;
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                                                                                                                                                                                                                                                                                                                                           ul-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Ul-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Hypotherical protein ECU09_1300.
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Last annotation update)
                                          29;
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16.9%; Score 68.5; D 26.2%; Pred. No. 12; ive 19; Mismatches
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                                                                                                                                                                                                     256 ERELLAVLGHELGHFVHKDI 275
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                                                                                                                                                                 55 RRKIVTYAGELLLQGVHDDV
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nes 29; Conserv
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RESULT 15
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Ramiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T19F11 genomic sequence."
"Arabidopsis thaliana chromosome III BAC T19F11 genomic sequence."
Submitteed (JAN-2001) to the EMBL,GenBank/DDBJ databases.
EMBL; AC009918; AAF02137.1;
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InterPro, IPRO00782, B19H3 fasciclin.
PF02469; Fasciclin; I.
SEQUENCE 447 AA; 49236 MW; B6CB1062AF267379 CRC64;
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                                                                                                                                                                                                                                                                                                         DB 10; Length 447;
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1-MR-2002 (TrEMBLrel. 20, Last annotation update)
AT3311700/T1911_10 (Hypothetical 50.8 kDa protein)
T19F11.10/AT3317700.
                                                                                                                                                                                                                                                                                                      16.6%; Score 67.5; DB 10;
35.7%; Pred. No. 18;
iive 8; Mismatches 11;
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Hypothetical protein.
SEQUENCE 462 AA; 50792 MW.
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tes 20; Conserv
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN-CV. LANDSBERG;
Pittman J.K., Hall J.L., Williams L.E.;
"Identification of Nramp5, a heavy metal transporter in Arabidopsis
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;; Pred. No. 33;
11; Mismatches 36; Indels
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Mayer K.F.X.;
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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PRODOM; PD001861; Nramp; 1.
TIGRFAMS; TIGR01197; nramp; 1.
SEQUENCE 530 AA; 58781 MW; 837E2D22F1BB2E37 CRC64;
                                                                                                                                         Ion transporter-like protein (Heavy metal transporter) F28A21.200 OR AT4G18790 OR NRAMP5.
                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
  530 AA
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

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Title: Perfect score: Sequence:

US-09-648-310-1 780 1 gycacgagctctcctcgtcc.....gtaataaaaaaatcatgt 780

IDENTITY_NUC Gaport 1.0 Scoring table:

2054640 seqs, 14551402878 residues Searched:

Total number of hits satisfying chosen parameters:

4109280

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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GenEmbl:* Database :

em_hum:* gb_htg:* gb_in:* gb_om:* gb_un:* gb_vi:* em_ba:* Fun∃_me b_sts:1 gb_pat:* gb_ph:* gb_pl:* gb_ro:* b_sy:* em_mu:* em_om: gb_ba:* poor:

em_ph:* em_pl:* em_ro:* em_or: em_sts em_ov: em_pat

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em_htg_pln:* em_htg_rod:* em_htg_mus:

em_htgo_other:* _htgo_hum:* _htgo_mus:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AX456990 Sequence	117858	055 Rattus	91	505 Rattus	Mus mus	Wus mus	Sednenc	sed n	ACLIVOYO MUS HIGGE	omen c	Homo		Sednen	AC129055 Rattus no			S	la	lastocyst	.latifoli	Arabidop	Arabid	Oryza	HOHO		5139 Rattu	7663 Caenorh	5803	702 Caeno	8 Homo sap	45 Plasmod	2124 Sequenc	48889 Sednenc	0291 Rattus	228	7586 Clostri	5250 Rattus	3755 Rattus	8461 Rattus n	ISI33 Kat	_
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ALIGNMENTS

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	linear							Vertebrata;	Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae;	
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o c	dq na/	Sequence 1 from Patent WO0216419.		5783				Chordata; (Rodentia; 8	
		1 from Pat	AX456990	1 · GI:2171				; Metazoa;	Eutheria;	
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AX456990	rocus	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			

PAT 06-JUL-2002

RESULT 1

Fisher, P.B., Kang, D.C. and Su, Z.Z. Progression suppressed gene 13 (psgen 13) and uses thereof REFERENCE AUTHORS TITLE

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ilarity 100.0%; Pred. No. 5
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Patent: WO 0216419-A 1 28-FEB-2002;
The Trustees of Columbia University
Location/Qualifiers
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Nardy, D. A. Adman, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Albarcoks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarca, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Barbarca, J., Bowle, S., Briteva, M., Brown, E., Brown, M., Barks, T., Carrow, T., Burch, P., Burkett, C., Burnell, R.L., Byrd, N.C., Carrow, T. E., Carter, M., Cavazos, S. R., Chackon, J., Chwiez, D., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Cox, Coyle, M.D., Dathorne, S. R., David, R., Davis, C., Davy-Carroll, L., Dedarich, D. A., Davis, C., Davy-Carroll, L., Dedarich, D. A., Delaney, K.R., Derger, H., Dugan, Rocha, S., Lubin, R., J., Davis, C., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., Davis, C., Edwards, C.C., Elani, C., Edoar, D., Elani, C., Edoar, D., Elani, C., Edoar, D., Edwards, C.C., Elani, C., Edoar, D., Edwards, C.C., Elani, C., Edoar, D., Elani, C., Edoar, D., Edoar, D., Elani, C., Edoar, D., Elani, C., Harris, R., Harris, R., Harris, C., Mitcherge, D., Martin, C., Mitcherge, D., Martin, C., Liu, J., Liu, M., Loals, B., Lewis, L.C., Harson, E., Kallson, E., Martin, R., Martindale, A., Martinez, E., Maresh, A., Lacier, R., Laus, B., Lewis, L.C., Martin, C., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., More, C., Mose, M., Ren, C., Martin, S., Savery, G., Schergen, B., Sonalek, A., Tabor, Y., Vullalon, D., Vulles, M., Rolas, M., Rolas, A., Tabor, P., Parco, S., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Walliams, A., Walliams, A., Walliams, A., Walliams, A., Walliams, A., Walliams, A., Walliams
90548 bp DNA linear HTG 18-JUL-2002
***, 44 unordered pieces.
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On Jul 14, 2002 this sequence version replaced gi:20162682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3. (bases 1 to 90548)
                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                              AC117858.3 GI:21745767
HTG; HTGS_PHASE1.
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                                                         DEFINITION
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AUTHORS
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
OVDE: This is a "vorking draft' sequence. It currently
consists of 44 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                       ' NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                        Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
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Consensus quality: 51579 bases at least Q40
Consensus quality: 55476 bases at least Q30
Consensus quality: 58229 bases at least Q30
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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COMMENT

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Rattus norvegicus.
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Subtrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M. Banks, T., Barbaroks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M. Banks, T., Barbaroks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M. Banks, T., Barbaria, J. Benton, J. Binage, M.C., Barbaria, D. Bouck, J., Benton, J. Binage, M., Blankenburg, K. Bonnin, D., Bunky, C., Burrel, F.L., Byrd, N.C., Carron, P., Burkelt, C., Burrel, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chacko, J., Chako, J., Chang, C., Chen, T., Covale, M.D., Dathorne, S.R., David, R., David, R., David, C., Coyole, M.D., Dathorne, S.R., David, R., David, R., David, R., David, M.L., David, C., Enbal, C., Escortto, M., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Bing, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Hang, S., Durbin, K.J., Earibart, C., Edgar, D., Edwards, C.C., Elhaj, T., Foster, P., Frantz, P., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, M., Gunzathe, P., Hawes, A., Hernandez, J. Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hallins, F., Howard, S., Huber, J., Huly, S., Hawes, A., Hernandez, D., Hower, M., Holloway, C., Hollins, B., Jacobson, B., Jar, Y., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Martins, C., Martins, M., Mapua, P., Martins, M., Mattins, R., Mattins,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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           Morley, K.C. Direct Submission Submitted (25-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                             (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 70 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                                                                                        Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124518 bases at least Q40
Consensus quality: 133171 bases at least Q30
Consensus quality: 139212 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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Rattus norvegicus clone CH230-107J10, *** SEQUENCING IN PROGRESS ***, 108 unordered pieces.
AC105605
AC105605
AC105605.
TGS_PASE1.
Norway rat
          /protein_id="AAI.16773.1"
/db_xref="GI:16303307"
/translation="EPHFFYSINNIFWAAGLQFASCFDRMSSGCRNCLKNGLREQKL
FHTSRWSLPFPWILKNNRFCLFY"
159 c 108 g 226 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAAT 749
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                                                                                                              DB 10;
                                                                                                                                        82:
                                                                                                           Score 482.8; DB 10
Pred. No. 3.8e-117;
0; Mismatches 82;
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/product="unknown"
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Best Local Similarity 85.8%;
Matches 587; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
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                                                                                                                                       133930 TGCGAAAAAGCTTTTGTTTTTTTTTTTAAACCATTTTTTTAGTCTTTGCCACACTTGACACTTCGGT 133871
                                                                               134350 AGATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC 134291
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Unpublished
Unpublished
E 2 (bases 1 to 692)

KS Ganguly,K., Yang,L.F. and Reddy,P.K.
Direct Submission
AL Submitted (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC a Brooklyn, 450 (larkson Avenue, Brooklyn, NY 11203, USA
Location/Qualifiers
1. 692
                                                                                                                                                                               GTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCATGATGTTGTTGACATTGTATTGCTGCA
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1 (bases 1 to 692)
Ganguly, K., Yang, L.E. and Reddy, P.K.
A novel CDNA clone from mouse thymus cDNA library
             Score 550.4; DB 2;
Pred. No. 7e-135;
0; Mismatches 1;
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/db_xref="taxon:10090"
/tissue_type="thymus"
<1. .240
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             70.68;
99.88;
           Query Match 70.6
Best Local Similarity 99.8
Matches 551; Conservative
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          1. (Dasses 1 to 294830)

1. Alsprooks.S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarola, J., Benton, J., Blange, K., Blanke, B., Brown, B., Drakon, C., Dray, Cartol, J., Charcko, J., Chavez, D., Cleveland, C.D., Carton, T.C., Cox, C., Coyle, M.D., Dathorne, S. R., David, R., Delaney, K. R., Delaney, K. R., Delaney, K. R., Delaney, K. R., Delaney, R. R., Douthwalte, K., Davy-Carroll, L., Douthwalte, K., Douthwalte, K., Douthwalte, K., Douthwalte, K., Douthwalte, K., Garner, T., Garza, M., Gall, R., Gabisi, M., Gals, J., Gabisi, M., Gals, J., Garner, T., Gabisi, R., Gabisi, R., Gabisi, M., Garner, J., Garner, T., Gabisi, R., Gabisi, J., Gabisi, M., Garner, J., Huly, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Harris, C., Harris, K., Harris, K., Harris, K., Harris, K., Marth, R., Martindale, A., Martharis, E., Manhiney, E., Marthary, L., Landry, N., Leal, B., Lewis, L.C., Martin, R., Soctt, G., Spark, A., Spark, R., Stanley, H., Stone, H., Suder, R., Martin, R., Wan, R., Wan, R., Wan, R., Wan, R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 13, 2002 this sequence version replaced gi:18092828.

Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: GNHM
Center clone name: CH230-107J10
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  (bases 1 to 294830)
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 108 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Dipublished

Stren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastlen, V., Boguslavkly, L., Boukhgalter, B.,
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Lopham, K., Travers, M., Travis, N., Trigillo, J., Ye, W.J., Young, G.,
Direct Submission, C., Lammer, A. and Zody, M., Zahnou, J., Zembek, L., Zimmer, A. and Zody, M., Zonnell, S., Vol, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Direct Submission, C., Lammer, A., and Zody, M., Zahnou, J., Zamon, S., Shupsa, J., Chan, M., When, J., When, J., Warn, J., When, J., Warn, Warn, J., 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., Dewar, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
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                                       -TTATTTTTTTTTTTTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAG
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Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Eembek, L., Zimmer, A. and Zody, M.
                                                                                                                                               Submitted (1-AGC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17061342.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: 118269
Center clone name: 191_F_12
Center clone name: 191_F_12
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 171878 bases at least Q40
Consensus quality: 174256 bases at least Q20
Insert size: 167000; agarose-fp
Insert size: 167000; agarose-fp
Insert size: 167000; agarose-fp
Quality coverage: 7.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110: contig of 119 bp in length
120 219: gap of 100 bp
1284: contig of 1365 bp in length
1285 1684: gap of 100 bp
14019: contig of 42335 bp in length
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51949 175262: contig of 23314 bp in length
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44120 47141: contig of 3022 bp in length
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84: contig of 3685 bp in length
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47242 51149: contig of 3908 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 2455 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14: gap of 100 bp
73488: contig of 7344 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15362: gap of 100 bp
176083: contig of 721 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1957: gap of 100 br
151848: contig of 22891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οţ
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66044: contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51150 51249; gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83700:
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175363 1760
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Db 164344 AGATGCTGATGGAAAATTAAGTGTGAAGTTTGGGGTCCTCTTCCAGGATGACAGATGTGC 164403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 164584 ACTAACGTGAATTTCCTTATGTATTTTTATAGAACTTTGTAAACAAAGGGGGCTTGTTG 164643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 164464 ATACGCAGGGGAACTACTTTTGCAAGGTGTTCATGATGATGATGATTGTATTGCTGC 164523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 GTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCATGATGATGTTTGACATTGTATTGCTGCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 AAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGATTAATGTGGTTTGCAGATCTGGGGGTATCTGGTAAACTGGAATAATTAAGTTAAAGG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAGTCCTGTTTTATACCTTGGAGCAAAACATTACAATGTAAAAATAAACAAAACCTG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 ACAAACATGAAGTTCCTTATGTATTTTATAGACCTTTGTAAACAAAAGGGGACTTGTTG
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                                                                                 /clone_lib="RPCI-24 Male Mouse BAC"
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85.1%; Pred. No. 8.7e-91;
11ve 0; Mismatches 68;
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a 35961 c 36427 g 52675 t
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128958. .151848
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151949. .175262
/note="assembly_fragment"
175363. .176083
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/note="assembly_fragment"
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                                                                                                                         'note="assembly_fragment
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                                              /db_xref="taxon:10090"
/clone="RP24-191F12"
 Location/Qualifiers
                                                                                                                                          clone_end:SP6
vector_side:left"
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Best Local Similarity
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State (189170)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, N., Cooke, P., Dearellano, K., Dears, S., Collymore, A., Cook, N., Dears, C., Dearstallano, K., Dears, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand Plerre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R., Landers, T., Leohoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Merquis, N., Mathews, C., Macdonald, P., Major, J., Merquis, N., Mathews, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Naylor, J., Pollara, V., Raymond, C., Retta, R., Riebeck, M., Riley, R., Rise, C., Rogov, P., Seman, S., Severy, P., Spencer, B., Stanger-Thoman, N., Stolanovic, N., Strauss, N., Subramanian, A., Travis, N., Travis, N., Travis, N., Travis, N., Travis, N., Ve, M., Waynen, C., Viel, R., Vo, A., Wilson, B., Wu, X., Wayman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Ye, W.J., Young, G., Direct, Submission
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Mus musculus clone RP23-69K22, WORKING DRAFT SEQUENCE, 31 unordered
Db 164644 AGAAGTCCTGTTTTATACCTTGAAGCAAAACATTACAATGTAAAATAAACAAAACC--- 164700
                                                                                                                                                                                                                                                                                                                                                      DD 164758 TGTGAAAAAGCTTTTGTTCTTTAAACCATTCTTAAGACAATTTCTACAGGCACTTGACA 164817
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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                                                                                                                                                                                                                                                                                                                 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703 CTCCGTCAAAGTGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGT 762
                                                                                                                                                      D 164701 ---TATTATTTTTTTTTAGAAGGTAATTGGGAAATGTAGGTAATGAAACATTTTTGGAGG
                                                                                                                                                                                                                                                                                                       TGCGAAAAAGCTTTTGTTTTCTTAAACCATTCTT-----AGTCTCTGCCACACTTGACA
                                                                                                  TTATTTTTTTTTTTTTTCTTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGG
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AC102536.2 GI:22380841
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Birren, B., Nusbaum, C.
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REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS

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Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Schauer, S., Schupback, R., Stojanovic, M., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Travers, M., Vassiliev, H., Zembek, L., Zimmer, A. and Zody, M.

Zembek, L., Zimmer, A. and Zody, M.

Direct Submitsed (21-MG-2002) Whitehead Institute/MIT Center for Genome Submitted (21-MG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 21, 2002 this sequence version replaced gi:17061622.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: 118974
Center clone name: 69_K_22
Sequencing vector: Plasmid: n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 181583 bases at least Q40
Consensus quality: 185286 bases at least Q20
Insert size: 184000; agarose-fp
Insert size: 184000; agarose-fp
Consilty coverage: 6.8 in Q20 bases; sum-of-contigs
Quality coverage: 7.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wl.mit.edu
Contact: sequence_submissions@genome.wl.mit.edu
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of 1161 bp in length
100 bp
of 1571 bp in length
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[ 1342 bp in length
100 bp
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9745 11173: contig of 1429 bp in length
11174 11273: gap of 100 bp
11274 112891: contig of 1618 bp in length
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contig of 1305 bp in length
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contig of 1431 bp in length
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contig of 2170 bp in length
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24923: contig of 1719 bp in length
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12992 14773: cont
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8370: con
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14874 16304: con
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1066 1722:
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Jap of 100 bp 8: contig of 2615 bp in length gap of 100 bp 8: contig of 3480 bp in length gap of 100 bp 10: contig of 43562 bp in length
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.05243 120007: contig of 14765 bp in length
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132266 149030: contig of 16765 bp in length
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149131 182946: contig of 33816 bp in length
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023: gap of 100 bp
26589: contig of 1566 bp in length
889: gap of 100 bp
29318: contin
                                                 yap of 100 bp 18: contig of 2629 bp in length
                                                                                             p of 100 bp contig of 2631 bp in length
                                                                                                                          49: gap of 100 bp 34373: contig of 2224 bp in length
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/clone_lib="RPCI-23 Female Mouse BAC"
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26690. .29318
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vector_side:left"
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.: gap of
40668: ___68
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84330: cont
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                                                                                                                                    DD 142161 AGATGCTGATGGAAAATTAAGTGTGAAGTTTGGGGTCCTCTTCCAGGATGACAGATGTGC 142220
                                                                                                                                                                                   Db 142341 AGATTAATGTGGTTTGCATGGCTTGGTGTATCTGATAAACTGGAATAACTAAGTTAAAAG 142400
                                                                                                                                                                                                                                                                                                                                                                                                                        142460
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Primates; Catarrhini; Hominidae; Homo.
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Progression suppressed gene 13 (psgen 13) and uses thereof
Patent: WO 0216419-A 3 28-FEB-2002;
The Trustees of Columbia University in the City of New York (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CICCGTCAAAGTGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATAITATGTTTATGT 762
                                                                                                                 229 AAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC 288
                                                                                                                                                                                                                                                                                                                                                                                                          ---TATTATTTTTCTTAAGAAGGTAATGGGAAATGTAGGTAATGAAACATTTTGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAGTCCTGTTTTTATACCTTGGAGCAAAACATTACAATGTAAAAATAAAAAAACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGAAAAAGCTTTTGTTTTCTTAAACCATTCTT-----AGTCTCTGCCACACTTGACA
                                                                                                                                                                                                                                                    349 GTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCATGATGATGTTGACATTGTATTGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                         ACAAACATGAAGTTCCTTATGTATTTTTATAGACCTTTGTAAACAAAAGGGGACTTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          589 TTATTTTTTTTTTTCTTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGG
                                                    Length 189170;
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                                                                                   Indels
                                                  49.3%; Score 384.2; DB 2;
llarity 85.1%; Pred. No. 8.7e-91;
Conservative 0; Mismatches 68;
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Pred. No. 5.6e-78;
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29419. .32049
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 160 c 176 g 25:
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Sequence 3 from Patent WO0216419.
AX456992
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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HTG 10-APR-2002
SAMPLING.
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Pred. No. 5.6e-78;
0; Mismatches 218;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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llarity 69.1%;
Conservative
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539; Conserv
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fisher, P.B., Kang, D.C. and Su, Z.Z.
Progression suppressed gene 13 (psgen 13) and uses thereof
Patent: WO 0216419-A 6 28-FEB-2002;
The Trustees of Columbia University in the City of New Yor
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Sequence 6 from Patent W00216419,
AX456995 AX456995.1 GI:21715786
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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source

REFERENCE AUTHORS

JOURNAL FEATURES

TITLE

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 10 AX456995

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44 24436: contig of 693 bp in length

37 24536: gap of 100 bp

40 25339: gap of 100 bp

40 25339: gap of 100 bp

40 25339: gap of 100 bp

41 26941: gap of 100 bp in length

42 26941: gap of 100 bp in length

43 2742: contig of 701 bp in length

43 2742: gap of 100 bp

43 2742: gap of 100 bp

44 27642: contig of 703 bp in length

45 2845: contig of 703 bp in length

46 28545: gap of 100 bp

46 29239: contig of 694 bp in length

40 29339: gap of 100 bp
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30019: contig of oc. ...
30119: gap of 100 bp
30801: contig of 682 bp in length
02 30901: gap of 100 bp
02 31589: contig of 688 bp in length
...
1689: qap of 100 bp
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1689: contig of 688 bp in length
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70701 bp in length
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85 15884: gap of 100 bp
15884: gap of 100 bp
17334: contig of 689 bp in length
46 16645: gap of 100 bp
35 17434: gap of 100 bp
35 17431: contig of 689 bp in length
35 18231: gap of 100 bp
32 18231: gap of 100 bp
32 18231: gap of 100 bp
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19: gap of 10: pp 1n ....
323390: contig of 70: bp 1n ....
100 bp .... of 673 bp in length
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23: gap of 100 bp
36312: contig of 689 bp in length
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f 703 bp
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12: contig of
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           contig of
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17435 18131: conti
18132 18231: car of
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.0362 11066: cont
.1067 11166: gap of
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8: gap of
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11962 12646; c
12647 12746; gap
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Forreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacCanth, M., McEwan, P., McKernan, K., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Neil, D., O'Neil, D., O'Neil, D., Netta, R., Petta, R., Ruback, M., Riley, R., Schauer, S., Schupback, R., Staues, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wux, N., Wyman, D., Ye, W.J., Young, G., Chante, A., Mannell, D., Ye, W.J., Young, G., Chante, A., Stander, R., Tanders, M., Travis, N., Trigillo, J., Yassillev, H., Viel, R., Wilson, B., Wux, N., Wyman, D., Ye, W.J., Young, G., Chante, A., Myman, D., Ye, W.J., Young, G., Chante, A., Myman, D., Ye, W.J., Young, G., Chante, M., Milson, B., Wux, N., Wyman, D., Ye, W.J., Young, G., Chante, M., Mallen, M., Tande, J., Anderson, M., Milson, B., Wux, Myman, D., Ye, W.J., Young, G., Chante, M., Mallen, M., Tande, J., Anderson, M., Milson, B., Wux, Myman, D., Ye, W.J., Young, G., Chante, M., Mallen, M., Tander, A., and Zody, M., Milson, B., Wux, Myman, D., Ye, W.J., Young, G., Chante, M., Mallen, M., Tander, A., and Zody, M., Milson, W., Whyman, D., Ye, W.J., Young, Whither, M. M., Mallen, M., Tander, A., and Zody, M., Milson, W., Whyman, D., Ye, W.J., Young, Whyman, M., Tander, M., Mallen, M., Mallen, M., Whyman, M., Tander, M., Mallen, M., Mallen, M., Mallen, M., M., Mallen, M., Mallen, M., Mallen, M., M., M., M., M., M., M., M., 
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This record contains 83 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-ARR-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                                                     Mus musculus, clone RP23-383P11
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Center clone name: 383_P_11
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4684: co
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1: gap of 100 ...
17896: contig of 693 bp 11.
186: gap of 100 bp 
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52115: contig of 702 bp in length
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113: gap of 100 bp
54499: contig of 686 bp in length
899: gap of 100 bp
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89.0%; Pred. No. 1.2e-77;
ive 0; Mismatches 45
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Best Local Similarity
Matches 372; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44212
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1-876
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                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 170882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                         Insert size: 170000; agarose-fp
Insert size: 170482; sum-of-contigs
Quality coverage: 13.6 in Q20 bases; agarose-fp
Quality coverage: 13.6 in Q20 bases; sum-of-contigs
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                the accession number will be preserved.

1 107625: contig of 107625 bp in length
10726 111441: contig of 3716 bp in length
111442 111541: gap of 100 bp
1111442 120063: contig of 852 bp in length
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120164 161248: contig of 41085 bp in length
161249 161348: gap of 100 bp
161349 170882: contig of 9534 bp in length.
Location/Qualifiers
                                                                                                                           Sequencing vector: Plasmid; n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 consenus quality: 169805 bases at least 030 Consenus quality: 169800 bases at least 030 Consenus quality: 170139 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 334.2; DB 2;
Pred. No. 1.6e-77;
0; Mismatches 43;
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37012 c 37190 g 44751 t
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/note="assembly_fragment"
111542. .120063
/note="assembly_fragment"
120164. .161248
/note="assembly_fragment"
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clone_end:SP6
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                                                                                                                  Summary Statistics
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/clone="RP23-284K1"
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                                       code: WIBR
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Matches 371; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarhini; Hominidae; Homo.
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Department of Experimental Hematology, Institute of Radiation Medicine,
Beljing Taiping Road 27, Beljing 100850, P. R. China
                                                                                                               56383
                                                                                                                                                                                                                                                                  399 TATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGTATCTGGTAAACTGGAATAATT 458
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1-876
Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,
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                                                                   ACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAACTCTGAAAGCCGCAAAACGAAGGA
                                                                                                                                                                   AGATTGTTACGTACGCAGGAGGCTGCTTTTGCAAGGTGTTCATGATGTTGACATTG
                                                                                                                                                                                                                                                                                                                                                                     AAGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTTATAGACCTTTGTAAACA 513
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/db_xref="SPPREMBL:Q9P1F3"
/note="predicted protein of HQ2013"
/product="PRO2013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-2000 (Rel. 63, Created)
09-MAY-2001 (Rel. 67, Last updated, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/organism="Homo sapiens"
/clone="FLB7547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens PRO2013 mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; RNA; HUM; 876 BP
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: a Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7959862. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNYDHEVNLLVEEIHRLGSKNADGKLSVKFGVLFRDDKCANLFE
ALVGTLKAAKRRIVTYPGELLLQGVHDDVDIILLQD"
106 c 157 g 221 t
                                                                                                                                                                                                                                                                                                                                                                 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Stavanna Chan, Readman Chlu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzyuinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasia van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra
    Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                Direct Submission
Submitted (01-007-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
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                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
ONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .743
/organism="Homo sapiens"
/db_xref="tocusID:58527"
/db_xref="toxon:9606"
/clone="MGC:22978 IMAGE:4849571"
/tissue_type="Blood, natural killer cell"
/clone_lnst="NIH_MGC_106"
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/protein_id="AAH14953.1"
/db_xref="G1:15928977"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
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      Eukaryota; Metazoa;
                                            (bases 1 to 743)
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                                                                                                                                                                                                                                                                                                                               BC Cancer Agency
info@bcgsc.bc.ca
                                                               Strausberg, R.
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/protein_id="AmF71102.1"
/translation="MNVDHEVNLLVEEIHRLGSKNADGKLSVKFGVLFRDDKCANLFEA
LVGFLKAARRRKIVTYPGELLLQGVHDDVDIILLQD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC014953 743 bp mRNA linear PRI 29-OCT-2001
Homo sapiens, hypothetical protein PRO2013, clone MGC:22978
IMAGE:4849571, mRNA, complete cds.
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                                                                                                                                                                                                    42 TITCICITAGCCCGAACCACITCCTICTTCTGCTTGTTCCTCCCTAGGGCGCGGAAGCTG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCATTTTTTGTTTCTGGTAA 427
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                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                            TAGTCT--CTGCCACACTTGACACTCGGTCAAAGTGAGAAGCGAACTAAAGACCAACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGGAATAATTAAGTTAAAGGACAAACAT ---GAAGTTCCTTATGTATTTTATAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGTAAACAAAAGGGGA--CTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   547 AATCTATGTATGATGCTATAAAATAAATCCTATTATTTTTCTCAGGAATCTGGTTAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGTTACGTACGCAGGAGCTGCTTTTGCAAGGTGTTCATGATGATGTTGACATTGTAT
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                                                                                                                                                                23;
                                                                                                                      DB 17; Length
                                                                                                                                                                Indels
                                                                              BP; 333 A; 131 C; 167 G; 245 T; 0 other;
                                                                                                                                                              0; Mismatches 211;
                                                                                                                                           Pred. No. 4.7e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGGAAAATATTATGTTTATGTAATAAAAAA 773
                                                                                                                    41.1%; Score 320.4;
69.0%; Pred. No. 4.7
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BC014953.1 GI:15928976
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                                                                                                                                       Best Local Similarity
Matches 520; Conserv
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RESULT 14 BC014953 ACCESSION

KEYWORDS VERSION

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ORGANISM

133 ACATECHTCOCOMAGNICATION (CONTINUED IN	RP11-501K14 is from the library F of Pieter de Jong. For further de http://www.chori.org/bacpac/home.yECYOR: pBACG3.6 IMPORTAWN: This sequence is not tRP11-501K14 It may be shorter be sections only once, except for a The true left end of clone RP11-5 The true RP11-5 The true RP11-5 The true RP11-5 The true RP11		/ hote- 5767. / hote- 6062. / hote- 6165. / hote- 6165. / hote- 7746. / hote- 9703. / hote- 9703. / hote- 10429. / hote- 10429. / hote- 10429. / hote- 10429. / hote- 10429. / hote- 10897. / hote- 10897. / hote- 10897. / hote- 11361. / hote- 12850. / hote- 13850. / hot
		AGCAAACATTACAATGTAAAATAAACAAACCTGTTATTTTTTTT	AL590308 100296 bp DNA linear PRI sequence. AL590308 AL590308 AL590308 GI:14596398 BOW Sapiens EUKATYOCIA: Metazoa; Chordata; Craniata; Vertebrata; Eute Uno 200296) BLAKEY, S. DIRCCT Submission Submitted (03-UL-2001) Sanger Centre, Hinxton, Cambridg Calford, W. E-mail enquiries; humquery@sanger.ac.uk Clrequests; clonerequest@sanger.ac.uk On Jul 4, 2001 this sequence version replaced gi:1425246 During sequence assembly data is compared from overlappin Where differences are found these are annotated as variatory ariation annotation may not be found in the sequence succertesponding to the overlapping clone, as we submit sequence was finished as follows unless otherwise norted annotation and as described above. This sequence was finished as follows unless otherwise norted by small overlap as described above. This sequence was finished as follows unless otherwise norted by the quality data (i.e., phred quality as mall overlap and repeats; all regions were covered by an expensions and repeats; all regions were covered by one plasmid subclone or more than one Mi3 subclone; and assembly was confirmed by restriction digest. The follow abbreviations are used to associate primary accession number to be found at the heat assembly was confirmed by restriction digest. The follow abbreviations are used to associate primary accession number the feature table with their source databases can be found at the heat assembly was generated from part of bacterial clone contigs of hutch mas generated from part of bacterial clone contigs of hutch from part of bacterial clone at the contrast of http://www.sanger.ac.uk/RGP/Chr6

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the entire insert of clone a 100 base overlapping a 100 base overlap. 1-501K14 is at 1 in this sequence. 255E12 is at 98297 in this sequence. 1-94L3 is at 97304 in this sequence.
RPCI-11.2 constructed by the group details see e.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atches 2242. .2323 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atches 2242. .2317 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atches 5863. .6175 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tches 5114. .5126 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tches 129. .279 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atches 90. .281 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nes 2607. .2709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nes 1768. .1916 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atches 45. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tes 2587. .2709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atches 21. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                               ches 103. .194 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atches 2. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atches 3. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thes 194. .256 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nes 962. .2419 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atches 1. .79 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ches 21. .166 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nes 821. .962 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ches 14. .151 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ches 7. .185 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tt 100% conserved"
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Fri

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7052...27421
/note="THELC repeat: matches 1. .369 of consensus"
27806..28116
/note="Alux repeat: matches 1. .309 of consensus"
28722...29109
/note="LIMD2 repeat: matches 5302..6111 of consensus"
/note="Alux repeat: matches 1. .310 of consensus"
29709...29708
/note="LIMD2 repeat: matches 1. .310 of consensus"
29709...29861
/note="LIMD2 repeat: matches 5164..5302 of consensus"
30862..31350
/note="HERVL repeat: matches 4611..5143 of consensus"
31360...31887
                                                                                                                                                                                                        // Acte="Miss repeat: matches 799. .865 of consensus" 23216. .23317 repeat: matches 3. .98 of consensus" // Acte="Lirsa repeat: matches 3. .98 of consensus" 23306. .23808 repeat: matches 46. .611 of consensus" 23306. .24586 // Acte="Miss repeat: matches 2. .802 of consensus" 24777. .25093 // Acte="Alusx repeat: matches 1. .312 of consensus" 25177. .25474. .27651 // Acte="Tirsa repeat: matches 1. .370 of consensus" 25474. .27051 // Acte="Tirsa repeat: matches 2. .1580 of consensus" 25474. .27051
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note="LTR16A repeat: matches 91. .444 of consensus" 33322
                                                                                                                                                                                                                                                                                                                                                                                                                                        note="L2 repeat: matches 2351, .2547 of consensus"
2027, .22320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "note="AluJb repeat: matches 1. .297 of consensus"
23321. .22369
10104="L2 repeat: matches 2547. .2593 of consensus"
2394. .22607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note "Alusx repeat: matches 1. .286 of consensus" 3717. .34028
16229. .16532
/note="%lusx repeat: matches 1. .301 of consensus"
16577. .16796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2749 of consensus
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15384. .35496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluJb repeat: matches 3. .311 of consensus"
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/note="MIR repeat: matches 32. .147 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .247 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .310 of consensus"
                                                                                                                                                     .149 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2982. .23029
note-"6 copies 8 mer gaaagaaa 79% conserved"
                                                                                                             .88 of
                                                                       .217 of
                                                                                                           /note="MEK58C repeat: matches 40.
18586. .18687
/note="MIR repeat: matches 48. .1
19512. .20572
                                                                       Ή.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3030. .23106
hote="L2 repeat: matches 2667.
3146. .23213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="AluY repeat: matches 1.
34911. .35200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MIR repeat: matches 32.
2674. .22981
                                                                 /note="MER20 repeat: matches
18247. 18407
                                                                                                                                                                                         note-"CpG island"
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                                                                                                                                                                                                                                             Gaps
                                                                                    /note="Alusx repeat: matches 11. .310 of consensus" 38644. .38737 /note="L2 repeat: matches 2616. .2717 of consensus" 700te="Aluso repeat: matches 4. .310 of consensus" /note="Aluso repeat: matches 4. .310 of consensus" /note="THELA repeat: matches 1. .353 of consensus" 41414. .41703
       /note="Alusx repeat: matches 1. .302 of consensus" 37165. .3720
/note="7 copies 8 mer tccttcct 75% conserved" 3727. .37266
/note="MIR repeat: matches 211. .250 of consensus" 38122. .38421
                                                                                                                                                                                                                                                                      AAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC
                                                                                                                                                                                                                                                                                                                                           75226 GTATGATGCTATAAATAAATCCTATTATTTTTCTCAGGAATCTGGTTAGGAATTGCAGG
                                                                                                                                                                                                                                                                                                                           349 GTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCATGATGTTGACATTGTATTGCTGCA
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                                                                                                                                                                                                                Length 100296;
                                                                                                                                                                                                                29.0%; Score 226.2; DB 9; Length 69.0%; Pred. No. 6.9e-49; ive 0; Mismatches 153; Indels
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Search completed: January 17, 2003, 01:34:22 Job time : 3838 secs

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/dev_stage="4 weeks"
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The WashU-HHMI Mouse EST Project
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/clone="IMAGE:948898"
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//lab_lost="wettor"
//lab_lo
                           1 (bases 1 to 51)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scence, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marrah, N., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R.,
Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (brownefas harvard.edu)
MGI:1948459 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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Pred. No. 2e-104;
0; Mismatches 45
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Other_ESTs: id05d03.x1
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Best Local Similarity 92.0%;
Matches 504; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 617-495-1812
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 593)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelsing,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA544950 S93 bp mRNA linear EST 04-AUG-1997 vk38e06.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:948898 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone is available royalty-free through LLNL ; contact the
                                      IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                         472 AACAIGAAGTICCTIAIGIAITITIAIAGACCTITIGIAAACAAAAGGGGACTIGIIGAGA
                                                                                                                                   AGTCCTGTTTTTATACCTTGGAGCAAAACATTACAATGTAAAAATAAAACAAAACCTGTTA
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Contact: Marra MyMouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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0271-10 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 600)
Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
21671825
Contact: Klein WH
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/clone_lib="Mouse E14.5 retina lambda 2AP II Library"
/tissue_type="neural retina"
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TTTTTTTTTTTTCTTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGC
                                                                                                                                                                                                                                                                                                                     Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117; 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
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HI/91389 551 bp mRNA linear EST 12-MAR-2002 id05d03.yl Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus cDNA clone IMAGE:5662133 5' similar to TR:081881 081881 BYPOTHETICAL 18:3 KD PROTEIN: ;, mRNA sequence.
/dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps
(Manniatis); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCACTGAATTCTGACTG----, Other
information regarding entire library may be found at
thtp://pga.swmed.edu/Data/Libraries/microarray_cdna_librar
ies htm "
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 1.4e-107;
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Best Local Similarity 89.0
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 613)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: embryo; Vector: pSPORT; Site_1: Not!; Site_2: Sal1; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: Sal1(dT): 5'-CGTCGACCGTTTTTTTTTTTTTTTTTT.3' CDNAS were cloned into the Not!/Sal1 sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger
                                                                                                                                                         AA607954 613 bp mRNA linear EST 30-SEP-1997 vm41a03.rl Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:992716 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:564996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Knowles Solter mouse blastocyst B1"
/tissue_type="blastocyst"
/de_stage="embryo (pre-implantation)"
/lab_host="bH10B"
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Unpublished (1996)
Contact: Marra MyNouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                724 ACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAA 773
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0; Mismatches 72;
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/organism="Mus musculus"
/strain="C57BL/6J x DBA/2J Fl"
/db_xref="texon:10090"
/clone="IMAGE:992716"
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Location/Qualifiers
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591 bp mRNA linear EST 30-JUL-1997
vj80b03.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone
ILMAGE:035309 5', mRNA sequence.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Martin,J., Milson,R., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                 467
                                                                                                                                                       527
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                                                                                                                                                                                                                                                                                     418
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                                                                                     648 GIGCGAAAAAGCITITGITITCITAAACCATICIT ----- AGICICIGCCACACITGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                      702 ACTCCGTCAAAGTGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTTATG
                                                                                                                                                                                                                                        GAGAAGTCCTGTTTTATACCTTGGAGCAAAACATTACAATGTAAAAATAAAACCT
                                                                                                                                                                                                                                                                                                                            GTTATTTTTTTTTTTTTCTTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra Myduose EST Project
Washb-HHMI Mouse EST Project
Washb-HHMI University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fars: 314 286 1810
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/db_xref="taxon:10090"
/clone="IMAGE:935309"
/clone_llb="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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Location/Qualifiers
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Similarity
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ORIGIN
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        T 3'); double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE687862 669 bp mRNA linear EST 11-SEP-2000 uw52c09.x1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone INAGE:3465616 3' similar to TR:081881 081881 HYPOTHETICAL 18.3 KD BE687862.
                                                                                                                                                                7
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                TGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 ACAAAACCIGITATITITITITITITAGAAGGTAATCGGGAGACGTAGGCAATAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -TAGACAAGACCTATTATTTTTTTTAAGAAGTACTTGGGAAATGTAGGTAATGAAAGA
                                                                                                                                                                7;
                                                                                                                                             Score 455; DB 9; Length 593;
Pred: No. 5.8e-104;
                                                                                                                                                               Indels
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                                                                                                                                                                0; Mismatches
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 'lab_host-"DH10B"
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                                                                                                                                             58.3%;
88.5%;
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                                                                                                       Bonaldo."
                                                                                                                                                               518; Conservative
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                                                                                                                                                      Similarity
                                                                                                                182
                                                                                                                                             Query Match
                                                                                                                                                      Best Local
Matches 51
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BE687862/c
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                                                                                                                SASE COUNT
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/cissue_type="mammary gland"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
/note="Vector: pT73D-pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4,
                                               Project (CGAP),
                                                                                                                               Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1384976
High quality sequence stop: 389.
Location/Qualifiers
1. 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    610 TACCCTCTTGGTGAAGGAAATTCATCGCCTGGGTTCCAGAAATGCTGATGGAAAATTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGT
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1 (bases 1 to 669)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:3465616"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.9%; Score 452; DB 10;
ilarity 85.4%; Pred. No. 3.2e-103;
Conservative 0; Mismatches 80;
                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                               Tumor Gene Index
Unpublished (1997)
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313 239 371 299 359

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CITGITCCICCCIAGGGGGGGGGGAAGCIGAGGGGGGGGTTCAGACCCACGCGGGGGAGCAGC 133
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                                                                                                                                                                                 CTCCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                    314 ACT-CTGAAAGCCGCAAAACGAAGGAAGATTGTTAC-GTACGCAGGAGAGCTGCTTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 AAGGTGTTCATGATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 GGGGGTATCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACATGAAGTTCCTTATGTA
           Pred. No. 4.8e-94;
0; Mismatches 51; Indels
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High quality sequence stop: 4
Location/Qualifiers
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Unpublished (1997)
Other_ESTs: uw52c09.x1
      89.28;
                               494; Conservative
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        Best Local
Matches 49
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KEYWORDS
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AUTHORS
TITLE
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/clone="IMAGE:5710372"
/clone="IMAGE:5710372"
/clone="IMAGE:5710372"
/clone="IMAGE:5710372"
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/dev_stage="embryo 15:5 dpc"
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/lab.host="DH10B (Tl phage resistant)"
/lab.host="Drain: Vector: Pix7-Asc; Site_1: EcoR I;
Site_2: Not I: The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
CDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, disested with Not I, and then
cloned directionally into pix7-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
intoretry of Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lu Dupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Councing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                  BQ445291 547 bp mRNA linear EST 29-MAY-2002
UI-M-ERO-bxn-b-05-0-UI.rl NIH_BMAP_ERO Mus musculus cDNA clone
IMAGE:5710372 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , is GTGCGTGGAA. This ilbialy was created and only project diversity of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 547)
                                                                                                                                                                      TGGGGGTATCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACATGAAGTTCCTTATGT
                                                                                                       369 TIGGIGIATCIGATAAACIGGAATAACTAAGTTAAAAGACTAACGIGAATITCCTIAIGI
                                                                                                                                               491 ATTTTTATAGACCTTTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTATACCTT
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1. .547
/organism="Mus musculus"
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                                                                                                                                                                                                                                                             GGAGCAAACATTACAATG 569
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BE689324 504 bp mRNA linear EST 11-SEP-2000 uw52c09.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3465616 5' similar to TR:081881 081881 HYPOTHETICAL 18.3 KD
                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musil hases 1 to 504)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 507).

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Materston, R.

The WashD-HHMI Mouse EST Project
Unpublished (1996)

Contact: Marra M/Mouse EST Project
WashIngton University School of Medicinep
WashIngton University School of Medicinep
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@atson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                        T 3'), on equal amounts of mRNA from 2 13.5dpc and 2
State Univ. Tom 2 1 3 double stranded by Minoru Ko, Wayne
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT773 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 CTGCTTGTTCCTCCCTAGGGCGGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGCGAGC 130
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                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:439056"
/clone_lib="Soares mouse embryo NDME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       507;
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                                                                                                                                                                                                                                                                                                               1. .507
/organism="Mus musculus"
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High quality sequence stop: 359.
Location/Qualifiers
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Matches 456;
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                                                      (Pharmacia
                                                                                                                                                                                                                                                                       'n
                                                  /note="Organ: mammary gland; Vector: pT/T3D-Pac (Pharmac
) with a modified polylinker; Site_1: Not I; Site_2: Ecc
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
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                                                                                                                                                                                                                                        Length 591;
                                                                                                                                                                                                                                                                   55; Indels
                                                                                                                                                                                                                                        Score 425; DB 9;
Pred. No. 2.1e-96;
            /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                        54.5%;
88.7%;
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Matches 496; Conservative
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Genome Res. 6 (9), 791-806 (1996)
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                                                                                        Jobe "Vector: pr773D-pac (Pharmacia) with a modified polylinker: 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. ** 80 c 123 g 144 t l others
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGATTGTTACGTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCATGATGATGTTGACATT
                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                               DB 10; Length 504;
                                                                                                                                                                                                                                                                                           Indels
/db_xref="taxon:10090"
/clone="IMAGE:3465616"
/clone_llb="Soares_mammary_gland_NMLMG"
                                                                                                                                                                                                                                                             53.2%; Score 414.6; DB 10; ilarity 91.6%; Pred. No. 8.6e-94; Conservative 0; Mismatches 40;
                                             /sex="female (lactating)".
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACAAAACCTATTATTTTTTT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAAAACCIGITAITITII 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse,
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                               Best Local Sim
Matches 460;
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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BF468668
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KEYWORDS
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/db_xref="taxon:1000"
/db_xref="taxon:1000"
/clone="UI-M-BHAP_MS4"
/clone="II-M-BHAP_MS4"
/clone="II-M-BHAP_MS4"
/dev_stage="27-3 days"
/lab_host="DT-32 days="DT-32 days="DT-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                     it
of
                                                                                                                                                                                                                                     Email: mESTemail.nih.gov
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS.
Should be noted that Bento Soares is generating a small number o additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 TTCTGCTTGTTCCTCCCTAGGGCGCGGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGGGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 GCAGCTCTTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTAACCTCCTGGTGGAGGAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAACTGA 248
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Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
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Pred. No. 1.5e-93;
0; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collaborative arrangements
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J
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Matches 448; Conservative
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Search completed: January 17, 2003, 02:00:47 Job time: 2236 secs
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ORIGIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA linear EST 01-FEB-2002 CDNA Library Mus musculus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368
                                                                                                                                                                                                                                                                                TGCAAGGTGTTCATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGA 428
TTAACCTCCTGGTGGAGGAAATTCATCGCCTGGGTTCCAGAAATGCTGATGGAAAATTAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Genetics
National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnad[gsun.grc.nia.nih.gov
Plate: L0506 row: D column: 12
Seq primer: -21M13 Forward
                                                                                  Systematic Analyses of NIA Mouse Newborn Heart cDNA Library
Unpublished (2001)
                                                                                                                                                                                             GTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGG
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/tissue_type="Newborn Heart"
/dev_stage="Newborn"
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/db_xref="niaEST:L0506D12-3"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM122169 580 bp
L0506D12-3 NIA Mouse Newborn Heart
clone L0506D12 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH108"
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KEYWORDS
SOURCE
ORGANISM
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BM122169/c
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JOURNAL
COMMENT
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site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with ligation mixture by the chemical method. The average insert size is about 1.8 kb. The library was constructed by Yulan Piao (NIA)."
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                                                                                                                                                                                        205 GGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGT
                                                                                                                                                                                                                                                                   TTGTAAACAAAAGGGGACTTGTTGAGAAGTCCTGTTTTTATACCTTGGAGCAAAACATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         683 ----AGTCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAGGGGAACTAAAGACCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACAATTTCTACAGGCACTTGACATTCTGTCAAAGCAAGAAGCAAACTGCAGACCAGCTG
                                                                                                                                                                                                         CCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAACTCTGAAAGC
                                                                                                                                                                                                                                                                                                           CGCAAAACGAAGGAAGATTGTTACGTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCATGA
                                                                                                                                                                                                                                                                                                                                                                     385 TGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGTATCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                445 AAACIGGAATAATTAAGTTAAAGGACAAACAIGAAGTICCITAIGIATITITATAGACCI
                                                                                                                                                              14;
                                                                                                                               Length 580;
                                                                                                                               Score 406.6; DB 13; Length
Pred. No. 8.8e-92;
0; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGTGGAAAATATTATGTTATGTAATAAAAAA 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATGAAAAATGT--TGTTTATGGAATAAAAAAA 14
                                                                                                                             tch 52.1%; al Similarity 85.6%; 492; Conservative
                                                                                     Ø
                                                                                     177
                                                                                                                               Query Match
Best Local
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1 (bases I to 672)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H.
III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                   AW555045

L0249C06-3 NIA Mouse Newborn Ovary CDNA Library Mus musculus CDNA clone L0249C06 3', mRNA sequence.

AW555045

GI:7200468
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                 Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnadlgsun.grc.nia.nih.gov
Plate: LO249 row.c column: 06
Seq primer: -21M13 Forward
High quality sequence stop: 672
                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NIA Mouse Newborn Ovary cDNA Library"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
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Pred. No. 2.3e-109;
0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                      /db_xref="niaEST:L0249C06-3"
/db_xref="taxon:10090"
/clone="L0249C06"
                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Newborn Ovary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                      1. .672
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J
                                                                                                                                                                                                       Contact: George J. Kargul
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86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 86.4
Matches 577; Conservative
                                                                              Mus musculus
                                                                    house mouse,
                                                                                                                                                                                                                                                                                                POLYA-Yes.
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Best Local 8
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ORIGIN
                                           VERSION
KEYWORDS
SOURCE
ORGANISM
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COMMENT
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                                 ACCESSION
                                                                                                               REFERENCE
                                                                                                                           AUTHORS
                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                          TITLE
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                 /protein_id="Bab29100.1"
/db_xref="G1:12851887"
/db_xref="MGD:MG1:1920362"
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ALYGTLKAAKRRKIVTYAGELLLQGVHDDVDIVLLQD"
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                                                                                                                                                                                                                                                                                              140 GTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCTCCTG 199
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                                                                                                                                                                                 19;
                                                                                                                                                          DB 11; Length 769;
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                                                                                                                                                         Score 539.2; DB 13
Pred. No. 3.6e-125
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                                                                                                                                                                               0; Mismatches
                                                                                                                         221
                                                                                                                        174 g
                                                                          746. .751
/note="putative"
769
                                                                                                          /note="putative"
146 c 174
          /codon_start=1
                                                                                                                                                        69.1%;
86.6%;
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                                                                                                                                                                     Similarity
                                                                            polyA_signal
                                                                                                                                                                     Best Local Simi
Matches 658;
                                                                                                  polyA_site
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AW555045/c
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Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, W., Casatalov, P., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schrimil, L.M., Stabuli, F., Suzuki, R., Tomita, M., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninoi, P., de Bonaldo, M.F., Brownstein, M., Bult, C., Fletcher, C., Fujita, M., Gariboli, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Troyo-Oka, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.
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Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
Carninci, P., Fukuda, S., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,
Hume, D., Imotani, K., Ishli, Y., Ttoh, M., Izawa, M., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Konno, H., Koya, S.,
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,
Numazaki, R., Ohno, M., Okazaki, T., Okido, T., Owa, C., Quackenbush, J.,
Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Schrini, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamanuka, I.,
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNs was primed with a primer [5' GAGAGAGAGATCCAAGAGCTTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 50.0. Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, VRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Plaese visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of sequence [5' GAGAGAGATTAATTAAATTCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SatI. Cloning sites, 5' end: XhoI; 3' end: SstI.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155. .400
/note="data source:SPTR, source key:Q9P1F3, evidence:ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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/db_xref="Fan70m_DB:3110003A17"
/db_xref="MGD:MGI:1906054"
/db_xref="taxon:100090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK013984 150 bp mRNA linear HTC 19-JAN-2002 Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110003A17:homolog to PR02013, full insert sequence.
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Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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TCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAAAAGACCAACTGCGGTGG
                                                                                        AAACTGGAATAATTAAGGTTAAAGGACAAACATGAAGTTCCTTATGTATTTTATAGACCT
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                                                                                      /dev_stage="addit"
/lab_host="bhl0B (Life Technologies)"
/lab_host="bhl0B (Life Technologies)"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DRI
library is a normalized Rat Osteoblast library (nREO)
constructed in pT3T7 vector according to the procedure
described by Bonaldo, Lennon & Soares (Normalization and
Subtraction: Two Approaches to Facilitate Gene Discovery.
Genome Research 6: 791-806, 1996). The oligonucleotide
used to prime first strand synthesis contained the
sequence tag AAGATATCAA between the Not I cloning site and
dT18 stretch. The Rat Osteoblast Lissue was provided by
Lian & Stein of the University of Massachussetts Medical
tail. The sequence tag present in the cDNA between the NotI site and the Oligo-dT track Served to verify it as a clone from the normalized osteoblast library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: MI3 Forward POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 646; DB 14;
Pred. No. 4.7e-152;
0; Mismatches 5;
                                                                                                                                                  /clone="UI-R-DR1-ckz-m-14-0-UI"
/clone_lib="UI-R-DR1"
                                                                                                              /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                             230
                                                                                                                           /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                       TAG_LIB=UI-R-DR1
TAG_TISSUE=osteoblast
                                                                                                                                                                                                                                                                                                                                                                                TAG_SEQ-AAGATATCAA"
163 c 109 g
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Best Local Similarity 99.0%;
Matches 661; Conservative
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Best Local
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AA891725 642 bp mRNA linear EST 08-JAN-1999 EST19528 Normalized rat kluney, Bento Soares Rattus sp. cDNA clone RKIAGO2 3' end, mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee, N. H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Kat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT/T3Pac; Site_l: EcoRI;
Site_2: Not1"
155 c 99 g 204 t
                                                            772
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713 GTGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAA
                                                                            92 GTGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 642;
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/db_xref="taxon:10118"
/clone="RKIAG02"
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Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
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Shop woder

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AA607954
AA542157
AA008262
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A7186148
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AAS44950 vk38e06.r BEB687862 uw52c09.x AA607954 vm41a3.r AA608262 uw52c09.x BC45291 UT-M-ERO-BE689324 uw52c09.y BR468668 U1A-BH3-BR122169 LO506D12-AL134666 ud37d02.r AR220360 mv70d02.r AR220360 mv70d02.r AR220360 mv70d02.r AR33412 u6186403.x BR49249 BB849249 BB849249 AA220360 vv60d08.r AA816139 vv60d08.r AA816139 Vv60d08.r AA83425 uc82e12.x AA816230 vf90f10.r AA96660 uc82e12.x AA124233 EST230921 AF11662 Homo sapi BR161398 Homo sapi BR110495 602386283 AA986611 uc82d03.y BR1110495 60289473 BG228919 60259350 AV16363 AV716363 AN16363 AV716363

ALIGNMENTS

RESULT

AW492391 BG164526 AW027019

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AI133406

٥	BQ192542 690 bp mRNA linear EST 30-APR-2002	UI-R-DR1-ck2-m-14-0-UI.s1	UI-R-DR1-ckz-m-14-0-UI 3', mRNA sequence.		BQ192542.1 GI:20368093	EST.	Norway rat.	SM Rattus norvegicus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	Rattus.	3. 1 (bases 1 to 690)	S Bonaldo, M.F., Lennon, G. and Soares, M.B.	Normalization and subtraction: two approaches to facilitate gene	_	Genome Res. 6 (9), 791-806 (1996)		Contact: Soares, MB	Program for Rat Gene Discovery and Mapping	University of Iowa	451 Eckstein Medical Research Building Iowa City, IA 52242, USA	Tel: 319 335 8250	Fax: 319 335 9565	Email: msoares@blue.weeq.ulowa.edu	The sequence contained an oligo-dT track that was present in the	oligonucleotide that was used to prime the synthesis of first
BQ192542/c	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM				REFERENCE	AUTHORS	TITLE		JOURNAL	MEDLINE	COMMENT								

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_other:*

em_gss_mam:*

em_gss_fun:

em_gss_vrt:

em_gss_hum:* em_gss_inv:*

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gb_est3:*
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gb_est5:*
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em_gss_rod:

SUMMARIES

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AK013984 AW555045 BG804701 BI791389

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646 636 539.2 476.4 469.4

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BQ192542 AA891725

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Query Match Length

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Description

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Gaps 0;
                                                                              229 AAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGC 288
                                                                                                                                             289 CAATCICITIGAAGCGITGGIGGGAACTCIGAAAGCGGGAAAACGAAGGAAGAITGTIAC 348
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14.1%; Score 109.6; DB 21; Length 657;

Best Local Similarity 67.5%; Pred. No. 1.1e-20;

Matches 154; Conservative 0; Mismatches 74; Indels 0;
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146 GCCATGAACGTGGAGGAGGAGGTCGGGAGGCTCAAGGAGGAGATCCATAGGCTCGGCCAG 205
                     286
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                                                                                     227 AAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGT
                           Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 75315.
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GCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCATCTGGGTTCC 226 167

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Gaps

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DB 21; Length 551;

14.78; 67.28;

Matches 162; Conservative

Similarity

Local

99US-0135124. 99US-0135353. 99US-0135629.

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                                   AAC53910 standard; DNA; 551 BP
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(ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mealitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to novel genes (ABAll004-ABA21534) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 119.6; DB 22; Length 351; 66.0%; Pred. No. 1.2e-23; ive 0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 73; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 351 BP; 104 A; 72 C; 103 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0251160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.3
Best Local Similarity 66.0
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-541565/60.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-2000; 2
11-DEC-2000; 2
05-JAN-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-2000;
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89; Indels

87 AGGGCGCGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGCGAGCAGCTCTTCAGTGAAGA 146

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150 GAAAACCGCGCAGAAGGCAGCAACAATGTGGATCACGAGGTTAACCTCTTAGTGGAGG 209

147 AGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGG

AAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCC 266

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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirhemmatic; hepatotropic; cerebroprotective; antiinflammatory; antialleratc; antiidiabetic; antiincer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss
    260 AAATGCTGATGGAAAGTTAANTGTGAAAATTGGGGTCCTCTTTCGTGATGATAANTGAGC 319
                                        Human nervous system related polynucleotide SEQ ID NO 73.
                                                                                                                                                                                   ABA11066 standard; cDNA; 351 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001; 2001WO-US01334
                                                                                                                                                                                                                                                                    23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MAR-2000;
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                                                                                                                                                                                                                             ABA11066;
                                                                                                                                              RESULT 13
                                                                                                                                                                    ABA11066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       called human colon career antigens, juven in AAB3234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disoases such as neural disorders, immune system disorders, muscular disorders, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC97991 to AAC98763 encode the human colon cancer associated proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                               identification; cytostatic; cardioactive, neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 AATGAACGIGGAGCAIGAGGITAACCICCIGGIGGAGGAAAIICAICGICIGGGIICCAA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAIGCCGAIGGGAAACIGAGIGIGAAGIIIGGGGICCICTICCAAGACGACAGAIGIGC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colon cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                        Human colon cancer antigen nucleotide sequence SEQ ID NO:318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 388 BP; 109 A; 70 C; 95 G; 84 T; 30 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 764; 2104pp; English.
              AAC98308 standard; cDNA; 388 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders such as colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000; 2000WO-US05883.
                                                                                               09-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-587534/55.
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                                                                                                                                                                                                                                                                                                                                                                                     WO200055351-A1.
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000
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Matches 156;
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                                                         AAC98308;
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                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229
AAC98308
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is a fragment of the progression suppressed gene 13

(PSGen13). This gene has suppressed expression in progressed tumour cells. PSGen13 was identified using new methods for identifying nucleic acids differentially expressed between two samples. The method involves performing reciprocal subtraction differential RNA display (RSDD) between the two samples. The subtraction samples are amplified and compared to identify those nucleic acids that are differentially expressed the method is used to identify and clone of inferentially expressed genes, particularly those with increased or reduced expression during tumour cell progression, e.g. progression suppressed genes (PSGen) and progression elevated genes (PSGen). The method reduces the complexity of the band pattern produced in mithod reduced suppression and progression subtern produced in conventional differential RNA display (where bands may be obscured, resulting in false positive signals) since most bands common to both samples are eliminated allocations of genes and pattern produced in and progression and common to both samples are eliminated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying nucleic acids differentially expressed between two samples, particularly sequences involved in tumour progression
663 TGTTTTCTTAAACCATTCTTAGTCT - - CTGCCACACTTGACACTCCGTCAAAGTGAGAAG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             displaying anticipated differential expression. RSDD requires only a single anchored primer for amplification and reamplified cDNA can be
                                                                                               Progression suppressed gene; PSGen; progression elevated gene; tumour; reciprocal subtraction differential RNA display; RSDD; differential expression; gene cloning; cancer; ss.
                                                                                                                                                  721 CGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAAAA 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.1%; Score 157; DB 20; Length 177; larity 100.0%; Pred. No. 2.5e-34; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                          Fragment of progression suppressed gene 13 (PSGen13).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analysed by reverse Northern blotting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examples; Fig 23; 110pp; English.
                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0032684.
98US-0185115.
98US-0197889.
                                                                                                                                                                                                                                                                                                 AA221551 standard; DNA; 177
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-1998;
03-NOV-1998;
23-NOV-1998;
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    683
                                                                                        743
                                                                                                            61 GTCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAAAGACCAACTAGCGGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    684 GICICIGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAAAGACCAACTGCGGTG 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of isolating and identifying differentially expressed nucleic acids between two samples by using a reciprocal subtraction differential display (RSDD) method. This sequence represents clone PSGen-13 which is a novel gene.
GTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCTTAAACCATTCTTA
                    GTCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAGCGAACTAAAGACCAACTGCGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying differentially expressed nucleic acids between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.1%; Score 157; DB 20;
100.0%; Pred. No. 2.5e-34;
ive 0; Mismatches 0;
                                                                                                                                                                                             744 GAAAATATTATGTTATGTAAAAAAAAAATCATGT 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAATATTATGTTATGTAATAAAAAAATCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by reciprocal subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples; Fig 23; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK,
                                                                                                                                                                                                                                                                                                                         AAX25869 standard; cDNA; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0032684.
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone PSGen-13 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-214060/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fisher PB;
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RESULT 12

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Gaps

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Indels

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The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribosyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins of the invention.

Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New colon cancer polypeptides and polynucleotides, useful as vaccines, for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 GTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAACTCTGAAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 GCCGCAAAACGAAGGAAGATTGTTACGTACGCAGGAGAGCTGCTTTTGCAAGGTGTTCAT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 CATTITITGTTTCTGGTAAACTGGAAT-ATAAAGTGAAAGAACAAACATTTGAACATACT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT---GAAGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 TAATGTATTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGCCTGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             603 TTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTATGTATTTTTATAGACCTTTGTAAACAAAAGGGGA--CTTGTTGAGAAGTCCTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24; Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.5%; Score 206.6; DB 24; Length 68.7%; Pred. No. 4.4e-48; 1ve 0; Mismatches 144; Indels
    Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 552 BP; 190 A; 104 C; 75 G; 183 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                               Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 939; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Xu J,
                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-223283P.
28-MAR-2001; 2001US-279763P.
29-JUN-2001; 2001US-302051P.
                                                                                                                                                                                                          31-JUL-2001; 2001WO-US24218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 68.7
Matches 366; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-241739/29.
                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
                                                                                                                  WO200212328-A2.
                                                                         Homo sapiens.
                                                                                                                                                               14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                             King GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                         expressed in cancer tissues. ABB78993 to ABB79004 represent proteins expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABB60775 to ABB78993 to ABB79004 represent proteins canced by the ABB60775 to ABB78097 nucleic acid sequences. (I) can be used in antisense therapy An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate maroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTCCAAGACGACAGATGTGCCCAATCTCTTTGAAGCGTTGGTGGGAACTCTGAAAGCCG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386
                                                                                                                                                                                    Molino GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 AGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAACGAAGGAAGATTGTTACGTACGCAGGAGCTGCTTTTGCAAGGTGTTCATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGITGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGGGGTATC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 215.6; DB 24; Length 627;
Pred. No. 1.3e-50;
0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dwivedi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 627 BP; 171 A; 151 C; 153 G; 147 T; 5 other;
                                                                                                                                                                                  Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA encoding colon tumour protein, SEQ ID
                                                                                                                                                                                  Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.6%; Sccilarity 83.3%; Pre
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 796pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK45388 standard; cDNA; 552
                                          02-OCT-2001; 2001WO-US30732
                                                                                        02-OCT-2000; 2000US-237271P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                     Thiaglingam A, Lewis ME;
                                                                                                                                                                                Astle JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 245; Conservat
                                                                                                                                                                                                                                                  WPI; 2002-426115/45.
                                                                                                                                     (FARB ) BAYER CORP.
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11-APR-2002
                                                                                                                                                                                  Burgess C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK45388/c
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                                                                                                                                                                                                                                       AGGTGTTCATGATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTG 432
                                                                                                                                                                                                                                                             391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy -
                      Gaps
                                                           91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molino GA;
                                     73 GCTTGTTCCTCCCTAGGGCGCGGGAAGCTGAGTGCAGGGTTCAGACCCACGCGGCGAGCAG
                                                                           133 CTCTTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAA
                                                                                                                              ||| TAIGTACTGCCATTTTTGTTTCTGGTAAACTGGAAT-ATAAAGTGAAAGAACAATT
                                                  CCTCCTGGTGGAGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGT
                                                                                                                                                                                                 GGGGTA-------TCTGGTAAACTGGAATAATTAAGTTAAAGGACAAACAT-
                                                                                                                                                           GAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; colon cancer; cancer; tissue profilling; forensic; mapping; genetic analysis; diagnostic; antisense therapy; gene; ss.
                     19;
   Length 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  related nucleotide sequence SEQ ID NO:748.
                                                                                                                                                                                                                                                                                                                              Dwivedi P,
                    93; Indels
                                                                                                                                                                                                                                                                                                                  477 --GAAGTICCTIAIGTAITITIAIAGACCTITIGIAAACAAAAGGGGACI
 21;
Score 252.2; DB 2
Pred. No. 6.8e-61;
0; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 796pp; English
32.3%;
76.1%;
                                                                                                                                                                                                                                                                                                                                                                                       ABQ57053 standard; cDNA; 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2001; 2001WO-US30732.
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                  Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burgess C, Astle JH,
Thiaglingam A, Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-426115/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FARB ) BAYER CORP.
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200229086-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon
                                                                                                                                                                                                                                                                                                                                                                                                          ABQ57053;
 Query Match
                                                                                                                                                                             212
                                                                                                                                                                                                                   272
                                                                                                                                                                                                                                       373
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                                                                                                                   193
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ABQ57053
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB7893 to ABB79004 represent proteins encoded by the ABQ60775 to ABB060787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoractive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and concleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of colls from a patient. (I) is useful for determining the presence of coln cancer in a cell or tissue type, for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate acroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise attibodies, and to screen for peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                      TGTTCCTCCCTAGGGCGCGCGAAGCTGAGGGGTTCAGACCCACGCGGCGAGCAGCTC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGAAAGCCGCAAAACGAAGGAAGATGTTACGTACGCAGGAGGGCTGCTTTTGCAAGG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGITCATGATGATGTTGACATTGTATTGCTGCAA - - GATTAATGTGGTTTTGCAGATCTGG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGCGGGAAGGAAAACCGCGCAGAAGAAGGAATGAATGTGGATCACGAGGTTAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTTGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAGCGTTGGTGGGAAC
                                                                                                                                                                                                                                                                                                           DB 24; Length 717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon cancer related nucleotide sequence SEQ ID NO:557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, colon cancer, cancer, tissue profiling, forensic, r
genetic analysis, diagnostic, antisense therapy, gene, ss
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                          Sequence 717 BP; 192 A; 171 C; 155 G; 180 T; 19 other;
                                                                                                                                                                                                                                                                                                          Score 250.4; DB 24;
Pred. No. 2.2e-60;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                       32.1%;
ilarity 75.6%;
Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ56862/c
ID ABQ56862 standard; cDNA; 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 ATGIACC 474
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                                                                                                                                                                                                                                                                                                                            Best Local Sim
Matches 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ56862;
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                       16
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and correcting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a coll. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a coll. A probe/primer derived from (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molino GA;
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                                                                      Human; colon cancer; cancer; tissue profiling; forensic; mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysis, mapping and diagnostic applications. (I) can be used tantibodies, and to screen for peptide analogues and antagonists.
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Human colon cancer related nucleotide sequence SEQ ID NO:750
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                                                                                                                 genetic analysis; diagnostic; antisense therapy; gene; ss
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Matches 323; Conservative
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Thiaglingam A, Lewis
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                                                                                                                                                                                            Homo sapiens
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Sequence 712 BP; 241 A; 121 C; 149 G; 201 T; 0 other;
                                                                        Parkinson's diseases and cancers -
                                                                                                         Claim 1; Page 336; 423pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and parasitic infections.
P-PSDB; AAB32005
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidaterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiavascular disorder; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
                   The invention relates to the isolation of genes AAC66410-C66458 encod 49 human secreted proteins AAB32002-B32050. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes a proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and overlan cancer and other cancers of the adrenal gland, bone, bon marrow, breast, gastrointestinal tract, liver, lung, or urogenital:

(b) immune disorders e.g. Addison's disease, allergies, autoimmune
376 TGTTCATGATGATGATGACATTGTATTGCTGCAAGATTAATGTGGTTTGCAGATCTGGGG
                                                                                                                                                                                                                                                                                                                             Human secreted protein coding sequence SEQ ID NO: 14.
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                                                                                                                                                                                                             AAC66413 standard; DNA; 712 BP.
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99US-0171552.
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                                                                           436 GTATC 440
                                                                                                               465 GTACC 469
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Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                  641
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                                                                                                                                                                                                                                                                          642 ATTITCTCAGGAAICTGGTTAGGAATTGCAGGCAATGAGATTTTTGCGGGCAGGGAT 701
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                                                                                                                                                                                                                                                                                                                                                                                        Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
343 TCTTAAAGCTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAGCTGCTTCTGCAAGG
                                                                                                                                         AAGTTCCTTATGTATTTTTATAGACCTTTGTAAACAAAAGGGGACT--TGTTGAGAAGTC
                                                                                                                                                                                                                                                       596 TTTTTTTTTTAAGAAGGTAATCGGGAGACGTAGGCAATAAAATGTTTTCAGAGGTGCGAAA
                             376 IGTTCATGATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGGTTTGCAGATCTGGGG
                                          AAGCTTTTGTTTTCTTAAACCATTCTTAGTCT - - CTGCCACACTTGACACTCCGTCAAAG
                                                                                                                                                                                                                                                                                                                                           GGGAATGTTTGTTCATAAATAATTAGACATTTTCTATAGATATTTGACATTCTGCGAAAG
                                                                                    ACATACTTAATGTATTTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGT
                                                                                                                                                                                                                            CTGTTTTTATACCTTGGAGCAAAACATTACAATGTAAAAATAAACAAAACCTGTTATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate cancer antigen nucleotide sequence SEQ ID NO:545.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 1004-1005; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders such as prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF16110 standard; cDNA; 778 BP
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wound; infectious disease; ss.
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(ROSE/) ROSEN C A.
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P-PSDB; AAB56907.
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            The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynuclectides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive,
called prostate cancer antigens, given in AAB56363 to AAB57302
                                                                                                                            disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195
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                                                                                                                                                                                                                                                                 DB 21; Length 778;
                                                                                                                                                                                                                                                              Score 288.2; DB 21; Length
Pred. No. 5e-71;
2; Mismatches 167; Indels
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                                                                                                                                                                                                                               Sequence 778 BP; 250 A; 151 C; 148 G; 221 T; 8 other;
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                                                                                                                                                                                                                                                            Query Match 36.9%;
Best Local Similarity 69.9%;
Matches 451; Conservative
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TCTGAAAGCCGCAAAACGAAGGAAGATTGTTACGTACGCAGGAGAGCTGCTTTTGCAAGG 375
                                                                                                                                                                                                       patients suffering from a cancer
                                                                                                                                     (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                      Claim 4; Fig 2; 53pp; English
                                                                                                                      25-AUG-2000; 2000US-0648310.
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Matches 539; Conservative
                                                                                                       27-AUG-2001; 2001WO-US26795
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                      Homo sapiens
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                                         CTTCCTTCTTCTGCTTGTTCCTCCCTAGGGCGCGGAAGCTGAGTGCAGGGTTCAGACCCA
                                                                                                                                  GGCACGAGCTCTCGTCCCTTCCTCCACTGCAGCCTTTCTCTTTAGCCCGAACCA
                                                                                             CGCGGCGAGCAGCTCTTCAGTGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGA
                                                                                                                                                         GAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTG-
                                                                                                                                                                                       AAGCGTTGGTGGGAACTCTGAAAG-CCGCAAAACGAAGGAAGATTGTTACGTACGCAGGA
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                                                                                                                            GCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAAATGCCGATGG
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      Length 800;
                    Indels
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     20;
           .3e-202;
     DB
                   Mismatches
    Score 754.8;
Pred. No. 1.3
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   tch 96.8%; al Similarity 99.5%; 778; Conservative
   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 TGTTCCTCCTAGGGCGCGCGAAGCTGAGGGGTTCAGACCCACGCGGCGAGCACTC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 TTCAGTGAAGAAGGAAGCAATCGAGGGTCAGCAATGAACGTGGAGCATGAGGTTAACCT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAAAATGCCGATGGGAAACTGAGTGTGAA 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 ATTTGGGGTCCTCTTCCGTGATGATAATGTGCCCAACCTCTTTGAAGCATTGGTAGGAAC 342
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                                                                                                                                                                                                                                                                          /product= "Progression suppressed gene 13 protein"
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blood vessel; nasopharyngeal tumour; thyroid tumour; leukaemia;
lymphoma; breast; lung; prostate; ovary; colon; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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69.1%; Pred. No. 2.9e-84;
tive 0; Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New rat and human Progression Suppressed Gene 13 growth of cancer cells and/or new blood vessels,
                                                                                                                                                                    Location/Qualifiers
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                                                                                                            RESULT 2
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                                                                                                                   rat or human progression Suppressed Gene 13 (PSGen 13) protein. The nucleic acids are useful for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer, cancer of the breast, lung, prostate, ovary or colon. PSGen 13 may also he used to suppress the transformed phenotype of a malignant cell. Administration of PSGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour marker, tumour metastasis, vascularisation, perfusion, or rate of tumour growth, improved clinical symptoms, and/or increased patient survival. The present sequence represents the coding sequence of rat Progression
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                                                                                                          The invention relates to novel isolated nucleic acids which encode a
                                                                                                                                                                                                                                                                                                                                                                                1 GCCACGAGCTCTCCTCGTCCCTTCTCCCACTGCAGCCTTTCTCTTTAGCCCGAACCA 60
                                  New rat and human Progression Suppressed Gene 13 for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCACGAGCTCTCCTCGTCCCCTTCTCCCACTGCAGCCTTTCTCTTTAGCCCGAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CGCGGCGAGCAGCTCTTCAGTGAAGAAGGAAGCAATCGGAGGGTCAGCAATGAACGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATGAGGTTAACCTCCTGGTGGAGGAATTCATCGTCTGGGTTCCAAAAATGCCGATGG
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100.0%; Pred. No. 1e-209;
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                         Suppressed Gene 13 (rPSGen 13).
                                                                                  2; Fig 1; 53pp; English
                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 780; Conservative
2002-280914/32
           P-PSDB; AAU76532
                                                                                  Claim
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has suppressed expression in progressed tumour cells. PsGeni3 was identified using new methods for identifying nucleic acids differentially expressed between two samples. The method involves performing reciprocal subtraction differential RNA display (RSDD) between the two samples to generate two subtraction samples. The subtraction samples are amplified and compared to identify those nucleic acids that are differentially expressed. The method is used to identify and clone differentially expressed genes, particularly those with increased or reduced expression and progression elevated genes (PEGen). The method reduces the complexity of the band pattern produced in conventional differential RNA display of the bands may be obscured, resulting in false positive signals) since most bands common to both samples are eliminated, allowing identification and reamplified requires only a single anchored primer for amplification and reamplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the progression suppressed gene 13 (PSGen13). This gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying nucleic acids differentially expressed between two samples, particularly sequences involved in tumour progression
                                                            720
                                                                                                                        780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEGen;
                              TTTGTTTTCTTAAACCATTCTTAGTCTCTGCCACACTTGACACTCCGTCAAAGTGAGAAG
                                                                                                                        /product= PSGen13
/note= "Progression suppressed gene 13 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Progression suppressed gene; PSGen; progression elevated tumour; reciprocal subtraction differential RNA display; differential expression; gene cloning; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Progression suppressed gene 13 (PSGen13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0032684.
98US-0185115.
98US-0197889.
                                                                                                                                                                                                                                                                                                                                                 AAZ21517 standard; cDNA; 800
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Clone PSGen-13 seq Human colon cancer

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Rat; Progression Suppressed Gene 13; rPSGen 13; cytostatic; cancer; blood vessel; nasopharyngeal tumour; thyroid tumour; leukaemia; lymphoma; breast; lung; prostate; ovary; colon; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Progression suppressed gene 13 protein"
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ABL72646
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/Na1981.DAT:*
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         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-87028234; PubMed-3533275;
Davis T.N., Urdea M.S., Masiarz F.R., Thorner J.;
"Isolation of the yeast calmodulin gene: calmodulin is an essential
                                                                                                                                                                                                                                                                                                                                                                                                     |: :: |:|::: | : :|:|
19 MSSAPKIELIVDKVASLSERRLEGRLPEDWFRHIMDPETEFNSEFADALCIGIDEFAQPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CMD1 OR YBR109C OR YBR0904.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Sąccharomycetaceae; Saccharomyces.
NCBL_TaxID-4933; .*
                                                                                                                                                                                                                                                                                          DB 1; Length 824;
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MEDLINE-87228267; PubMed-3295478;
Davis T.N., Thorner J.;
"Isolation of the yeast calmodulin gene using synthetic
                                                                                                                                                                                                                      FP (BY SIMILARITY).
5A5507544E06184C CRC64;
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                                                                                                                                                                                                                                                                                                            8; Pred. No. 40;
14; Mismatches
                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                 EMBL, X83413; CAA58369.1; -. Interper. Interper. Interper. Prop. Pfam; Pr02689; Herpes. Helicase; I. DNA replication; ATP-binding; Helicase.
                                                                                                                                                                                                                                                                                        14.8%; Score 60; 23.6%; Pred. No.
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01-JAN-1988 (Rel. 06, Last sequ
                                                                                                                                                                                                                                             93286 MW;
                                                                                                           EMBL; U13194; AAA68468.1; -. EMBL; X83413; CAA58369.1; -.
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Best Local Similarity 23.00,
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15-JUN-2002
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                                                                                                                                                                                                       -1- PTM: THE N-TERMINUS IS BLOCKED.
-1- MISCELLANEOUS: THIS PROTEIN HAS THREE FUNCTIONAL CALCIUM-BINDING
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                            MEDLINE=96424985; PubMed=8827436; Ohki S.-Y., Maura K., Saito M., Nakashima K.-I., Maekawa H., Yazawa M., Tsuda S., Hikichi K.; "Secondary structure and Ca(2+)-binding property of the N-terminal half domain of calmodulin from yeast Saccharomyces cerevisiae as studied by NMR.";
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                                                                                                                         J. Blochem. 119:1045-1055(1996).
-!- FUNCTION: CALMADOULIN MEDIATES THE CONTROL OF A LARGE NUMBER OI ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
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D->A: HIGHLY REDUCED AFFINITY FO

D->A: HIGHLY REDUCED AFFINITY FO

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W; 819EDIAD5D9400D3 CRC64;
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Pred. No. 6.8;
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EF-HAND 2.
EF-HAND 3.
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Job time : 81 secs
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InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 4.
ProDom; PD000012; EF-hand; 2.
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27.9%;
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PROSITE; PS00018; EF_HAND;
Calcium-binding; Repeat.
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                                                                                        - ADP + N-acetyl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus-6 containing homologues of human cytomegalovirus major immediate-early and replication genes.";
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                  osynthesis; Transferase; Kinase; Complete proteome.
257 AA; 27810 MW; 54EF26B46D6C064B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 LSVKFG--VLFQDDRCANLFEALVGTLKAAKRRIVTYAGELLLQGVHDDVDI 76
                                                                                                     DB 1; Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.8%; Score ov,
34.0%; Pred. No. 11;
+ive 8; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                   Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             824 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001048; Aa kinase.
InterPro; IPR004662; Acglukinase.
Plam; PF006965; aakinase; 1.
TIGRFAMS; TIGR00761; argB; 1.
Arginine biosynthesis; Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=95027704; PubMed=7941342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                EMBL; AP001118; BAB12772.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probable helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicholas J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U77 OR HDRF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELI_HSV6U
P52356;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
HELL HSV6U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
     à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                            Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylglutamate Kinase (EC 2.7.2.8) (NAG Kinase) (AGK) (N-acetyl-L-glutamate 5-phosphotransferase).
                                                                                                                                                              -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S9 KLHKWTQKKENGKKLSKMKVLLKHLTLANLLETLIVMPLDGMWNITVQWYAGELL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 (POTENTIAL).
CYTOPLESMIC (POTENTIAL).
N-LINELD (GLCNAC...) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 EIHRLGSKNADGKLSVKFGVLFQDDRCANLFEAL-VGTLKAAKRRIVTYAGELL 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.9%; Score 60.5; DB 1; Length 328; Best Local Similarity 36.4%; Pred. No. 13; Matches 20; Conservative 6; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                       PFam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

SR EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 (POTENTIAL).

EXTRACELIGIAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
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6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         EMBL; AF018072; AAC27099.2; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37648 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
84
                                                                                                                                                     MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 1
328 AA;
            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-TOKYO 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158
179
209
272
293
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SEQUENCE
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DOMAIN

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ARGB_BUCAI RESULT 13

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Gaps

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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.0%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32792; AAC22774.1; -.
                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equus caballus (Horse).
      Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
                                                                                     SEQUENCE FROM N.A.
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                                                      NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YAGELL 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRHR_HORSE
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GRHR_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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      à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AUTO-) (MAJOR SITE).
                                                                                                                                                                                                                                                                            -: - CATALYTIC ACTIVITY: AFP + a protein = ADP + a phosphoprotein. -: - PTM: Autophosphorylated. -: - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                              SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.

BELLINE-97256766; Pubmed-9099655;

Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M., Aebersold R., Pelech S.L.;

Identification of the autophosphorylation sites of the Xenopus laevis Pim-1 proto-oncogene-encoded protein kinase.";

J. Biol. Chem. 272:10514-10521(1997).
                                                                                                                                                                                                                                                                                                                            PIM SUBFAMILY.
CAUTION: Was originally (Ref.1) called Pim-1 but seems to represent the pim-3 isoform.
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.0%; Score 61; DB 1; Length 323; 32.6%; Pred. No. 11;
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PHOSPHORYLATION (AUTO-).
AB4DD61E7A99A38F CRC64;
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PHOSPHORYLATION (AUTO-).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
01sgoeptide transport ATP-binding protein oppf.
0PPF OR HI1120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FALSE_NEG.
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13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000001; Euk_pkinase; 1.
PROSTIE; PS00107; PROTEIN, KINASE_ATP; F.
PROSTIE; PS00108; PROTEIN, KINASE_ST; 1.
PROSTIE; PS50011; PROTEIN, KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 VAKER--VTEWG--TLNGVMVPLEIVLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AAKRRIVTYAGELLLQGVHDDVDIVLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36964 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L29495; AAA85389.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190
205
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54
69
168
                                                                                                                Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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205
323 AA;
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nes 29; Conserv
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                                                 PIM3 OR PIM1
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P45051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR OLIGOPEPTIDES. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE-95350630; Pubmed=7542800; Patrine of Medine of Section of No. 1, Millian of Section of No. 1, Millian of Section 
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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFORT SYSTEM (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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Pred. No. 11;
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Peptide transport; Transport; Inner membrane; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Indels
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45B6A3085431E3D9 CRC64;
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16-OCT-2001 (Rel. 40, Last annotation update)
Gonadotropin-releasing hormone receptor (GNRH-R).
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InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
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RESULT 11 OPPF_HAEIN

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Matches

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SUBUNIT: HOMODIMER.

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Van Montfort R.L.M., Pijning T., Kalk K.H., Hangyi I.,
Kouwijzer M.L.C.E., Robillard G.T., Dijkstra B.W.;
The structure of the Escherichia coli phosphotransferase IIAmannitol
reveals a novel fold with two conformations of the active site.",
Structure 6:377-388(1998).
-1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEDENDENT
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS HE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR): IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
PTS system, mannitol-specific ITABC component (EIIABC-MTL) (Mannitol-permease IIABC component) (Phosphotransferase enzyme II, ABC component) (EC 2.7.1.69) (EII-MTL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=KI2 / MG1655;
MFDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar - protein histidine + sugar phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugiyama J.E., Mahmoodian S., Jacobson G.R.; "Membrane topology analysis of Escherichia coli mannitol permease using a nested-deletion method to create mtlA-phoA fusions."; Proc. Natl. Acad. Sci. U.S.A. 88:9603-9607(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of the mannitol (mtl) operon in Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                        Lee C.A., Saler M.H. Jr., "Mannitol-specific enzyme II of the bacterial phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "S-phosphocysteine and phosphohistidine are intermediates in the phosphoenolpyruvate-dependent mannitol transport catalyzed by
                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                               system. III. The nucleotide sequence of the permease gene.";
J. Biol. Chem. 258:10761-10767(1983).
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                                                                                             637 AA.
116 NTTAEDIFQLGVKQSEGKLLVVFGPLGTD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 22:2576-2586(1994).
                                                                                             PRT;
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MEDLINE=88288055; PubMed=3135464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98212922; PubMed-9551558;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbiol. 2:405-412(1988).
                                                                                                                            21-JUL-1986 (Rel. 01, Created)
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                                                                                           STANDARD;
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                                                                                                                                                                                                                                                              Escherichia coli
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                                                      RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
          SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
PTM: AN INTRAMOLECULAR PHOSPHOTRANSFER TAKES PLACES BETWEEN
HIS-554 AND CYS-384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLF----EALVGTLKAAKRRIVTYAGE
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6
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Phosphotransferase system; Sugar transport; Transferase;
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                                             -1- SIMILARITY: CONTAINS 1 PTS EIIA DOMAIN-1- SIMILARITY: CONTAINS 1 PTS EIIB DOMAIN-1- SIMILARITY: CONTAINS 1 PTS EIIC DOMAIN
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                                                                                                                                                                                                                                                                            Ecogene; EG10615; mtlA.
InterPro; IPR004718; PTSIIC_mtlA.
InterPro; IPR002178; PTS_EIIA_2.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00359; PTS_EIIC.
Pfam; PF02378; PTS_EIIC; 1.
ProDom; PD001689; PTS_EIIA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         EIIC
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091822;
15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67972 MW;
                                                                                                                                                                                                      EMBL; V01503; CAA24748.1; -.
                                                                                                                                                                                                                     U00039; AAB18576.1; -.
                                                                                                                                                                                                                              EMBL; AE000438; AAC76623.1;
EMBL; X06794; CAA29953.1;
                                                                                                                                                                                                                                                                                                                                                                          IGRFAMS; TIGRO0851; mtlA; J
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PDB; 1A3A; 12-AUG-98
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637 AA;
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PIM3_XENLA
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                      VA maintenance in yeast requires a protein containing to the GTP-binding domain of dynamin.";
                                                                                                                                                                                                                                                                                                     STRAIN=FL100;
MEDLINE-93296170; PubMed-8516295;
Lalo D., Carles C., Sentenac A., Thuriaux P.;
Interactions between three common subunits of yeast RNA.polymerases I and III.";
                                                                                                                                                                                    Galisson F., Dujon B.;
Sequence and analysis of a 33 kb fragment from the right arm of
chromosome XV of the yeast Saccharomyces cerevisiae.";
Yeast 12:877-885(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.4%; Score 62.5; DB 1; Length 902; 25.6%; Pred. No. 23; Live 18; Mismatches 28; Indels 2
                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 90:5524-5528(1993).
-1- FUNCTION: REQUIRED FOR MITOCHONDRIAL GENOME MAINTENANCE.
-1- SUBCELLULAR LOCATION: Mitochondrial.
-1- SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transit peptide; Mitochondrion.
                                                                 SEQUENCE OF 60-902 FROM N.A.
MEDLINE-93365024; PubMed=7916673;
Guan K., Farh L., Marshall T., Deschenes R.J.;
"Normal mitochondrial structure and genome maintenance in requires the dynamin-like product of the MGMI gene.";
Curr. Genet. 24:141-148(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 ASP-RICH (ACIDIC).
245 GTP (POTENTIAL).
342 GTP (POTENTIAL).
409 GTP (POTENTIAL).
1150 G -> C (IN REF. 1 AND 2).
101523 MW; 89B8C745182AA5E8 CRC64;
                                                                                                                                                                                                                                                         Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION (POTENTIAL). MGM1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L07419; -; NOT_ANNOTATED_CDS. Z75119; CAA99426.1; -.
                                                                                                                                                              STRAIN-S288c / FY1679;
MEDLINE-9643797; PubMed-8840505;
MEDLINE-92192451; PubMed-1532158;
           Jones B.A., Fangman W.L.; Mitochondrial DNA maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001401; Dynamin.
Pfam; PF00350; dynamin; 1.
                                                                                                                                                                                                                                             SEQUENCE OF 179-902 FROM N.A.
                                                                                                                                                                                                                                                                                          SEQUENCE OF 734-902 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00410; DYNAMIN; 1.
MOTOR protein; GTP-binding; T
TRANSIT 7 902
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X92441; CAA63174.1; -. EMBL; L11274; AAB59316.1; -. EMBL; Z75120; CAA99428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X62834; CAA44637.1; -.
                                                                                                                                                   SEQUENCE OF 1-805 FROM N.A.
                                             3enes Dev. 6:380-389(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYNAMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00195; DYNAMIN SMART; SM00053; DYNC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dynamin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S33918; S33918.
PIR; S19068; S19068.
SGD; S0005737; MGM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
238
338
406
150
                                   region related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alexandre 5., Paindavione P., Tebabi P., Pays A., Halleux S., Alexandre S., Paindavione P., Tebabi P., Pays A., Halleux S., Steindrt M., Pays E.;

Steindrt M., Pays E.;

"Differential expression of a family of putative adenylate/guanylate cyclase genes in Trypanosoma brucei.";

Mol. Biochem. Parasitol. 43:29-288(1990).

-!- FUNCTION: COLLD ACT AS A RECEPTOR FOR A UNKNOWN LIGAND.

-!- CATALYTIC ACTIVITY: ATP = 3',5' cyclic AMP + diphosphate.

-!- SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Receptor-type ademylate cyclase GRESAG 4.1 (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i - SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 1; Length 1242;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452F8B22FFC0A2E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                   PRT; 1242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001054; G_Cyclase.
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
PROSITE; PS50125; GUANXLATE_CYCLASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
-----KRRKIVTYAGELLLQGVHDDVD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLLVEEIHRLGSKNADGKLSVKFGVLFQD 36
                                       774 GSEAIFLDKRCKVLSFRLKMLKNKCHSTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma brucei brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyase; cAMP synthesis;
DOMAIN 1 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1242 AA;
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=EATRO 1125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                       GRESAG 4.1.
                                                                                                                                                                                                CY41_TRYBB
Q99279;
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23; Conservative

Gaps

21;

28; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 HLRNILPPQAHQVAENSLNNLLKDKYKITYDKEATKNLAEKAVLAMENVKVSAEKNSVIV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 HEVNILIVEETHRIGSKNADGKLSVKFGVIFQDDRCANLFEALVGTLK----AAKRRKIVT 60
                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-96127529; Pubmed-8590279;
MEDLINE-96127529; Pubmed-8590279;
Sugiana M., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiana M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                          Synechocystis sp. strain PCC6803. I. Sequence features in the 1 N region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: TO B.SUBILLS YOFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerévisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.5%; Score 63; DB 1; Length 811; 22.1%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 18;
18; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL F6015BEBF804F255 CRC64;
                                                                                                           Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales; Saccharomycetaceae; Saccharomyces
      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGMI_YEAST STANDARD; PRT; 902 AA. P32266; Q08627; Q02609; 01-0cr-1993 (Rel. 27, created) 10-NOV-1997 (Rel. 35, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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MGM1 OR YOR211C OR YOR50-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002819; HD.
InterPro; IPR003607; ME_Pplase_HDc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00471; HDC; 1.
TIGREAMS; TIGR00277; HDIG; 1.
Hypothetical protein; Transme
                                                               Hypothetical protein slr0104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D64004; BAA10634.1; -.
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SEQUENCE OF 60-902 FROM N.A.
STRAIN-BJ41-8C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01966; HD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YAGELLLQ 68
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN*USDA 110spc4;
Bairl A., Mueller P.;
"sipF, the second functional type I signal peptidase of Bradyrhizobium japonicum, is encoded in the vicinity of essential genes involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLUTAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
-1- SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.6%; Score 63.5; DB 1; Length 231; Best Local Similarity 27.1%; Pred. No. 3.9; Matches 23; Conservative 15; Mismatches 30; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 EHEVNLLVEEIHRLGSKNAD-GKLSVKFGVLFQDDRCANLFEAL-------VGTLKA 52
                                                                                                                                                                                                                                                            Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7355F5A8039A4747 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Nuclease; Endonuclease; RNA-binding. DOMAIN 207 223 DRBM.
                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Ribonuclease III (EC 3.1.26.3) (RNase III).
                                                                                                                            231 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWART; SM00358; DSRM; 1.
SWART; SM00535; RIBOC; 1.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS50142; RNASE_3_1; 1.
PROSITE; PS50142; RNASE_3_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF065159; AAD02939.1; -.
InterPro; IPR001159; DS_RBD.
InterPro; IPR000999; RNase_3.
                                                                                                                                                           10-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 D
25071 MW;
                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=375;
:|||
124 WNDVD 128
                                                                                                                                                                                 30-MAY-2000
16-OCT-2001
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ID Y104_SYNY3
AC P54371;
                                                                                                                      RNC_BRAJA
069161;
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RESULT 6

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HDDVD 75
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P06331;
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifiad and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                            [1]
SEQUENCE FROM N.A.
SERINB-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-5637999; Pubmed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb L.M., Clayton R.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts R.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 IEHKVRDAFLLSEMLNAVG---RNGLFAVGIGICLEDDECIKIGNQILWEYKKNLINELK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87031575; PubMed-3095189;
Paces V., Vlcek C., Urbanek P., Hostomsky Z.;
"Nuclectide sequence of the right early region of Bacillus subtilis
phage PZA completes the 19366-bp sequence of PZA genome. Comparison
with the homologous sequence of phage phi 29.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
phi-29-like viruses.
NCBI_TaxID=10757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 44:115-120(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.0%; Score 65; DB 1; Length 432; 26.9%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Indels
Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
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432 AA; 48835 MW; 0EB95D188D2B41F3 CRC64;
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01-AUG-1988 (Rel. 08, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Early protein GP17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1- SIMILARITY: TO M. JANNASCHII MJ0977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003156; DHHA1.
InterPro; IPR001167; Ppesterase.
Pfam; PP01368; DHH; 1.
Pfam; PF02272; DHHA1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jannaschil.";
Science 273:1058-1073(1996)
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Best Local Similarity
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326 SVKLKKL 332
                                                                                                    NCBI_TaxID=2190;
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SEQUENCE 43
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P08389;
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V017_BPP2A
V017_BPP2A
V017_BP V017_BP
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DT 01-AUG-
DT 15-DEC-
DT 15-DEC-
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between the Swiss Institute of Bioinformatics and the FMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 LLEVTVEELGEQDNDDDLDEIDSELYEDAEASDVPHETIVKVFEADK -- SIVTFNGEKLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGEINHSGSTNY - - KTSLKSRVTISLDTSKNLFSLKLSSVTAAD - - TAVYYCARGLLRGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-85205332: PubMed-3922855;
Kudo A., Ishihara T., Nishihura Y., Watanabe T.;
*A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in 5' flanking region.";
Gene 33:181-189(1985).
PIK; A02101; G1HUH2.
HSSP: P01825; 7FAB.
InterPro; IPR0033006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANL-FEALVGTLKAAKRKIVTYAGELLL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 VEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVTYAGELLLQGV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                           Length 174;
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SIMILARITY: BELONGS TO THE PODOVIRUSES GP17 FAMILY.
                                                                                                                                                                                                                                                                                    PIR; F29004; WRBP70.
Early protein; DNA replication.
SEQUENCE 174 AA; 20022 MW; 08FBC8F91D4B4224 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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Pred. No. 2.1;
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15-VUL-1999 (Rel. 38, Last annotation update
119 heavy chain V-II region ARH-77 precursor.
Homo saplens (Human).
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D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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32.4%; Pred. No. 2.2;
ive 12; Mismatches
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(Rel. 06, Last seq
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hes 23; Conservative
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6; IGV; 1.
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Matches 22; Conserv
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| 120 HYVNVDVD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                  January 17, 2003, 01:34:28 ; Search time 78 Seconds (without alignments) 43.072 Million cell updates/sec
                                                                                                                                                                                                        406
1 MNVEHEVNLLVEEIHRLGSK......AGELLLQGVHDDVDIVLLQD 81
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P54371
P54371
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P00550
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P01822
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P08389
P06331
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Q9urv2
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y831_METJA
MC17_BPPZA
HY21_HUMAN
RNC_BRAJA
Y 104_SYNY3
MGML_YEAST
CY41_TRYBB
PTMA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSBI_ORYSA
ASTL_COTJA
FTSZ_THEMA
HELI_HSV6Z
RL27_BACSU
PME_PRUPE
PL10_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDX3_HUMAN
DDX3_MOUSE
CAPP_RHOPA
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YN8V_YEAST
ASB2_HUMAN
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HELI_HSV6U
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Maximum Match 100%
Listing first 45 summaries
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                                                                          - protein search, using sw model
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                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                      US-09-648-310-2
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Match
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<u> </u>	RESULT Y831_M ID Y AC O DT O DT 1 DE H	RESULT 2 Y831_METJA ID Y8311_ AC 05824 DT 01-NO DT 01-NO DT 16-OC DE HYPOU	LT 2 Y831_METJA Y831_METJA 01-NOV-1997 01-NOV-1997 Hypothetical MJ0831.	STAND (Rel. 35 (Rel. 35 (Rel. 40	STANDARD; 1. 35, Creat 1. 35, Last 1. 40, Last otein MJ0831	ID; Created) Last seq Last ann	PRT; d) equence nnotatio	432 AA. update) n update)			

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A;Residues: 1-2535 <BEV>
A;Cross-references: EMBL:AL035440
A;Cross-references: EMBL:AL035440
C;Genetics: Cultivar Columbia; BAC clone F10M23
C;Genetics: A;Map position: 4
A;Introns: 395/1; 613/3; 777/1; 826/3; 1945/2; 1993/3; 2061/3; 2129/3; 2178/3; 2295/3; A;Note: F10M23.350
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ë, Query Match 15.5%; Score 63; DB 2; Length 2535; Best Local Similarity 30.0%; Pred. No. 2.4e+02; Matches 27; Conservative 13; Mismatches 32; Indels 18; Gaps 2 NVEHEVN-----LLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAK 54 q δ

QQ

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Search completed: January 17, 2003, 02:17:36 Job time : 52 secs

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A; Map position: X
A; Introns: 87/3; 106/2; 151/3; 186/2; 210/3; 237/3; 268/3; 291/2; 334/1; 363/2; 404/3
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A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BAA10634.1; PID:d101
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T04824
R;Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes submitted to the Protein Sequence Database, February 1999
A;Reference number: 215385
A;Accession: T04824
                                                                                        C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Synechocystis Sp. A. Variety: P. P. Control F. C. Bools)
A.Variety: PCC 6803
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C.Accession: S76690
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C.Date: 23-Apr.1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 HEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLK----AAKRRKIVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPDB:GN00028
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Pred. No. 39;
4; Mismatches 13; Indels
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                                                               homolog - Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                        submitted to the EMBL Data Library, May 1996
A.Description: The sequence of C. elegans cosmid MO2A10.
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-514 <MIN>
A; Cross-references: EMBL:U58730; PIDN:AAC48058.1; GSPDE
A; Experimental source: strain Bristol N2; clone M02A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76690
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                                                                                                                                                                                                                                                                                                                               A, Accession: T29652
A, Status: preliminary; translated from GB/EMBL/DDBJ
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18; Mismatches
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Pred. No.
                                                        inward rectifier potassium channel
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ilarity 49.1%;
Conservative
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22.1%;
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                                                                                                                                                                                                                                                                                                  A; Reference number: 220659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 26; Conserv
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Best Local Similarity
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hypothetical protein -
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A; Residues: 1-811 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                        C; Accession: T29652
R; Minx, P.; Le, T.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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A;Gene: irk-2
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                                                                                                                                                                                                                                                                                                                                                               Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A:Accession: H72336
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-599 < ARN>
A:Cross-references: GB:AE001746; GB:AE000512; NID:g4981285; PIDN:AAD35852.1; PID:g498129
C:Genetics:
A:Genetics:
A:Genetics:
                                                                                                                                                                                                                                                                                                                           Hickey
                                                                                                                                                                                        C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
R;Accession: H7236
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Arabidopsis thalian imported fractions of C2 Species: Arabidopsis thalian imported fractions of C2 Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C; Accession: F64784 Film, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; R; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nierman, J. A.; Venter, J. A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nierman, J. A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nierman, J. A.; Venter, J. A.; Vent
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A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NVEHEVNLLVEEIHRLGSKNADGKLSV---KFGVLFQDDRCANLFEAL--VGTLKAAKRR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 VEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAK-RRKIVTYAGELLLQG 69
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                                                                                                                                                            conserved hypothetical protein - Thermotoga maritima (strain MSB8)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 2; Length 599;
Pred. No. 36;
9; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable glucosyl transferase [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 63.5; D
; Pred. No. 33;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Map position: 2
Superfamily: flavonol 03-glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470 ARISYHDPRMSLLEGVFSRGDRKLL 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 KIVTYAGE--LLLQGVHDDVDIVLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.8%;
36.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.6%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 VEKGGSSHSNITL-LLQD 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 V-----HDDVDIVLLQD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 15.8 Best Local Similarity 36.5 Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 32.1
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A; Residues: 1-496 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: F84784
A; Status: preliminary
124 WNDVD 128
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Best Local Si
Matches 25;
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C;Species: phage PzA A;Note: host Bacillus subtilis C;Species: phage PzA A;Note: host Bacillus subtilis C;Date: 31-Mar-1988 #text_change 23-Jul-1999 C;Accession: F29004 B;Paces, V; Vlcek, C; Urbanek, P.; Hostomsky, Z. Gene 44, 115-120, 1986 A;Paces, V; Vlcek C; Urbanek, P.; Hostomsky, Z. Gene 44, 115-120, 1986 A;Pacession: F29004 A;Pacesion: F290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Homo sapiens (man)
C.bate: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C.bate: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C.Accession: A03101.
R.Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
Gene 33, 181-189, 1889
A.; Tetle: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat se
A; Reference number: A02101; MUID:85205332; PMID:3922855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <sIG>
F;20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 IGEINHSGSTNY--KTSLKSRVTISLDTSKNLFSLKLSSVTAAD--TAVYYCARGLLRGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANL-FEALVGTLKAAKRRKIVTYAGELLL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 VEETHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVTYAGELLLQGV 70
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as Arg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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for residue 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 15.9%; Score 64.5; Di Local Similarity 32.4%; Pred. No. 7.9; nes 22; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;35-117/Domain: immunoglobulin homology <IMM>
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A, Note: the sequence was determined from the A, Note: the authors translated the codon GGG C, Genetics:
A, Gene: GDB:IGHV@
A, Cross-references: GDB:128528; OMIM:147070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;118-127/Region: D segment
F;128-146/Region: J segment
F;42-115/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 14q32.33-14q32.33
A; Introns: 16/3
early protein gp17 - phage PZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;20-117/Region: V segmen
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschif A;Reference number: A64300; MUID:96337999; PMID:8688087
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           Nypothetical protein ORF22 - ictalurid herpesvirus 1 (strain auburn 1)
C. Species: ictalurid herpesvirus 1
C. Species: ictalurid herpesvirus 1
C. Species: ictalurid herpesvirus 1
C. Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C. Accession: E36788
R. Davison, A.J.
S. Davison, A.J.
S. A. Reference number: A36804
A. Reference number: A36804
A. Residues: 1-1404 < CDAV>
A. Residues: 1-1404 < CDAV>
A. Residues: 1-1404 < CDAV>
A. Tesidues: 1-1404 < CDAV>
A. Title: Channel: addish virus: a new type of herpesvirus.
A. Reference number: A39447; MUID:92087490; PMID:1727613
A. Title: channel: adfish virus: a new type of herpesvirus.
A. Reference number: A39447; MUID:92087490; PMID:1727613
A. Contents: annotation
A. Molec. ineither protein nor nucleic acid sequence is given
C. Genetics:
A. Gene: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: FOR750952-752250
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                780 VEVRVNLLTEELART-KKTYDELRKLNNAYLTAKDRLQARVEALTTDNQSMKLLVGNGGT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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19;
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Pred. No.
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illarity 26.9%;
Conservative 15
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Best Local Similarity
Watches 26; Conserv
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Best Local Similarity
Watches 18; Conserv
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SVKLKKL 332
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44 EVSLLVE-----SKSDVKDGFNFVVLDQDQKQYESFCQDLFESRKGKDSLESVQKALK
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                                                                                             TRPF - - YAMMLLKKGFFDGV 114
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                                                         55 RRKIVTYAGELLLQGVHDDV 74
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Best Local Similarity 26.2%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-530 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                               C; Accession: F81343
                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: F81343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T04871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Sam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: Cj0723c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
                                                                                               97
                   셤
                                                       δ
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Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein MYPU_2370 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C.Species: Mycoplasma pulmonis C;Species: Ay.May-2001 *sequence_revision 24-May-2001 *text_change 03-Aug-2001 C;Accession: E99541
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A;Experimental source: strain UAB CTIP
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:235663; PIDN:CAA84722.1; GSPDB:GN00021; CESP:T04A8.4
A;Experimental source: clone T04A8
                                                                                                                                                                                                                                                                                                              hypothetical protein T04A8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24421
R:Palmer, S.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19889
A:Accession: T24421
A:Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                   Gaps
                                                                                       2 NVEHEVNLLVEEIHRLGSKNADG-KLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDR-----CANLFE-----ALVGTLKAAK 54
                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 20.1%; Score 81.5; DB 2; Length 289; Local Similarity 33.7%; Pred. No. 0.18; les 29; Conservative 14; Mismatches 26; Indels 1
              Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.0%; Score 69; DB 2; Length 318; illarity 36.2%; Pred. No. 4.9; Conservative 6; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels
        23.8%; Score 96.5; DB 2; Length 1 32.9%; Pred. No. 0.002; live 16; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 3
A;Introns: 26/2; 58/3; 102/3; 191/2; 223/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Genetic code: SGC3
C;Superfamily: phosphate acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: :| : ||:| | : | :|
111 RKYGLVHFEGEMLYQRQDDEXIITML 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 KRRKIVTYAGELLLQGVHDDVDIVLL 79
                                                                                                                                                                                                    61 YAGELLLQGVHDDVDIVLL 79
                             Similarity 32.9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-289 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <KUR>
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                                                   26;
            Query Match
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                               Best Local
Matches 2
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Matches
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A;Residues: 1-395 <PAR>
A;Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB72997.1; PID:g696
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F28A21.200 - Arabidopsis thaliana (5.5pc-loss; Arabidopsis thaliana (mouse-ear cress) (5.5pc-loss; Arabidopsis thaliana (mouse-ear cress) (5.5pc-loss) (5.7accession: T04871 (7.7accession: T04871 (7.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable integral membrane zinc-metalloproteinase Cj0723c [imported] - Campylobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 VSFMINLFVTAVFAKGFYGTKQADSIGLVNAGYYLQEKYGGGVFPILYIWGIGLLAAGQS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
96
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A;Note: F28A21.200
C;Superfamily: natural resistance-associated macrophage protein
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A;Experimental source: cultivar Columbia; BAC clone F28A21
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Pred. No. 7.1;
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January 17, 2003, 02:02:38; Search time 49 Seconds (without alignments) 158.916 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                             OM protein - protein search, using sw model
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US-09-648-310-2 406 1 MNVEHEVNLLVEEIHRLGSK.....AGELLLQGVHDDVDIVLLQD 81 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote				O)	hypothetical prote			_	Ig heavy chain pre	conserved hypothet	probable qlucosyl	inward rectifier p	hypothetical prote		probable glucosyl	probable glucosyl	methyl-accepting c	dynamin-like prote		_	phosphotransferase	glutamate-ammonia-	hypothetical prote	potential acrAB op	oliqopeptide trans	probable adhesin N	hypothetical prote	methyl-accepting c
SUMMARIES	ΩI	T04981	T21860	T24421	E90541	F81343	T04871	E36788	G64403	WRBP70	G1HUH2	H72336	F84784	T29652	876690	T04824	C84784	D84784	G64532	833918	AE2515	S14201	WOECZM	AE2697	E97479	AH0561	B64184	A81931	S	F71975
o#	Length DB	161 2		289 2				1404 2		174 1	146 1			514 2				496 2					637 1				332 2			
	Query Match I	70.4	23.8	20.1	17.0	16.9	16.3	16.3	16.0	15.9	15.8	15.8	15.6	15.5	15.5	15.5	15.4	15.4	15.4	15.4	15.3	15.3	15.1	15.1	15.1	15.0	15.0	15.0	15.0	14.9
	Score	286	96.5	81.5	ø	68.5	99	99	65	64.5	64	64			63	9	62.5	62.5	62.5	62.5	62	62	61.5	61.5	61.5	61	61	61	61	60.5
	Result No.	1	7	ю	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

hypothetical prote	procesn fronts:2 acetylqlutamate ki	3-hydroxyacy1-CoA	methionyl-trna syn	helicase [imported	calmodulin - yeast	metalloproteinase	cell division prot	U4/U6-associated R	U4/U6 small nuclea	hypothetical prote	hypothetical prote	galactoside transp	hypothetical prote	
F96560	D84935	D84286	D82249	T44037	MCBY	S41055	H72328	T50840	T50839	E69425	G64504	AH0183	C91188	C86035
0.0	9 79	~	7	~	-	~	~	7	~	~	7	7	~	7
573	257	629	731	824	147	310	351	682	683	775	287	206	637	637
14.9	14.8	14.8	14.8	14.8	14.7	14.7	14.7	14.7	14.7	14.7	14.5	14.5	14.5	14.5
60.5	60	09	09	09	59.5	59.5	59.5	59.5	59.5	59.5	59	29	29	29
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Search completed: January 17, 2003, 02:18:24 Job time : 37 secs ;;

DB 3; Length 660;

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|| | : | : | : | : | | | | 507 NVRHVINFOLPSDIEEYVHRIGRAGRUGL--ATSFFNERNMNITKDLLDLLVEAKQ 563
                                                                                                                                                                                                                                                                                                           2 NVEHEVNL----LVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKR 55
                                                                                                                                                                                                             13.4%; Score 54.5; DB 3; Length 6
27.1%; Pred. No. 69;
tive 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 NLLVEEIHRLGSK----NADGKLSVKFGVL-FQDDRCANLFEALVGTLKAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: SOOD NO. 621336thwestern Hwy., Suite 410 CITY: Parmington Hills STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tagle, Danilo A.
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE
NUMBER OF SEQUENCES: 24
ADDRESSEE: ROAD & ASSOCIATES
ADDRESSEE: ROAD & ASSOCIATES
STREET: 30500 No. 6211336thwestern Hwy., Suit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 TDYSVPCKRRKI-DVGWEVIKDYLQKSQSDFDLV 409
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EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 12, Application US/08952127
; Patent No. 6211336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 2290
TELECOMMUNICATION INFORMATION:
MENTION OF THE TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3066 amino acids
                                                                                                                                                                                                                                                            16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 48334
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Shiloh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                         LENGTH: 660
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                   US-09-058-489-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-952-127-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                     SEQ ID NO 91
                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                          13.4%; Score 54.5; DB 4; Length 128;
30.6%; Pred. No. 8.7;
Live 13; Mismatches 35; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        4 EHEVNLLVEEIHRLGS-----KNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 QYELEKILKENBELKAEKALSQMKNETRSMLNESGLENFDDQIVNI---LVNT-DAEKTR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NVEHEVNL----LVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WH197-08pA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 91, Application US/09058489
Patent No. 6103886
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Whitehead institute for Biomedical Research
APPLICANT: Whitehead institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Lahn, Bruce
APPLICANT: Lahn, Bruce
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WHI97-08PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.4%; Score 54.5; DB 3; Length 660; 27.1%; Pred. No. 69; tive 12; Mismatches 24; Indels
         CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PastSEQ for Windows Version 3.0
EED ID NO 18
LENGTH: 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/041,877
                                                                                                                                                                                                                                                  ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 KNVESFINLLNOMVKSNVEKALROD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 KIVTYAGELLLQGVHDDVDIVLLQD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-058-489-18
Sequence 18, Application US/09058489
Patent No. 6103886
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.6%
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 27.1%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Human
US-09-058-489-18
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US-09-058-489-91
                                                                                                                                                                                                      LENGTH: 128
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Length 3066;

; Score 54.5; DB 4; ; Pred. No. 4.7e+02; 16; Mismatches 28;

us-09-648-310-2.rai

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Sequence 4164, Application US/09134001C
Sequence 4164, Application US/09134001C
GENERAL INFORMATION:
APPLICAMT: Lynn boucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 VLLTVEENDSQKPQNADSKLPEDQLTPGDGHHVNRVFRPGLSDSTSAKSQVLFETEVSRK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SVKFGVLFQDDRCAN 41
                                                                                               16;
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                                                         Length 2206;
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                                                                                                                                                   30; Indels
                                                                                           8; Indels
                                                                                                                               ----RRKIVTYA---GELLLQGVHDDVDIV 77
                                                                                                                                                                                                                                                                                                                  APPLICANT: KAYE, FEDERIC J.
APPLICANT: OTTERSON, GREGORY A.
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF
TITLE OF INVENTION: NOVEL CHAPERONE PROTEIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 5: KNOBBE, MARTENS, OLSON & BEAR
620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/08/203,905B
FILING DATE: February 28, 1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 LF----NTLNEDLFQKILVPIQQVLKEGLLDKTEIDEVVL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 LFEALVGTLKAAKRRIVTYAGELLLQGVHD--DVDIVLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                       DB 4;
                                                   13.8%; Score 56; DB 4; 36.2%; Pred. No. 2e+02; ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: KIRKPATRICK, ANITA M.
REGISTRATION NUMBER: 32,617
REFERENCE/DOCKET NUMBER: NIH089.001A
                                                                                                                                                                                                                                                          Sequence 14, Application US/08203905B
Patent No. 5646249
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VNLLVEEIHRLGSKNADGKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.78; 27.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 472 amino acids TYPE: amino acid
                                               Query Match 13.8
Best Local Similarity 36.2
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92660
COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEWPORT BEACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                             47 VGTLKAAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                        US-08-203-905B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-203-905B-14
         US-08-465-250-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                      RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56; DB 2; Length 2206;
Pred. No. 2e+02;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 VGTLKAAK-----RRKIVTYA---GELLLQGVHDDVDIV 77
                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CAUREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/461,503
FILING DATE: 5-JUN-1995
                                                                                                                                                                                          36607-D-PCT-US
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,250
FILING DATE: 6-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release 1.30
                                                                                                                                           NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 3660;
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 278-0400
TELEFAX: (212) 391-0525
TELER: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2206 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08465250 Patent No. 6136570
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REMABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36f
TELECOMMUNICATION INFORMATION:
                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 13.8
Best Local Similarity 36.2
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-461-503-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                         FILING DATE: 5-CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Racani
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-465-250-2
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US-07-852-260-2
                                                                                                                                                                                                                 1870 VYRIGYKNSQNNTEKKLDLLVMENLFYGRKMAQVFD-LKGSL---RNRNVKTDTGK---- 1921
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                                                                                                                                                                                       14 IHRLGSKNADGKLSVKFGV----LFQDDRCANLFEALVGTLKAAKRRIVTYAGELLLQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 IHRLGSKNADGKLSVKFGV----LFQDDRCANLFEALVGTLKAAKRKIVTYAGELLLQ 68
                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 6406875el Mammalian Putative
Phosphatidylinositol-4-Phosphate-5-Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 56; DB 4; Length 2052;
; Pred. No. 1.8e+02;
15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/619,062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Harness, Dickey & Pierce, P.L.C. STREET: P.O. Box 828 CITY: Bloomfield Hills STATE: Michigan COUNTRY: U.S.A.
                                                                                                                                                     15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F
REFERENCE/DOCKET NUMBER: 4981-098431
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09619062
Patent No. 6406875
GENERAL INFORMATION:
APPLICANT: Shisheva, Assia
TITLE OF INVENTION: Phosphatidylin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,201
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.0%;
Matches 19; Conservative 15
                                                                                                              Ouery Match 13.8%;
Best Local Similarity 26.0%;
Matches 19; Conservative 19
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
.LENGTH: 2052 amino acids
LENGTH: 2052 amino acids
                   TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: unknown unknown
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1922 ---ESCDWLLDE 1931
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1922 ---ESCDVVLLDE 1931
                                                                                                                                                                                                                                                                    69 GVHDDVDIVLLQD 81
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                                                           ; TOPOLOGY:
US-09-045-201A-2
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Gaps
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                                                         APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2206;
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Patent No. 5834302

GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tacaniello, Vincent
APPLICANT: Tacaniello, Vincent
APPLICANT: Tacaniello, Vincent
APPLICANT: FROMINE METHODS FOR PRODUCING RNA VIRUSES
TITLE OF INVENTION: FROM CDNA
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
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                                                                                                                                                                                                                                                                                                                                                                     UPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/852,260
CLASSIFTAME: 19920619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB 1;
Pred. No. 2e+02;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19920619
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/JOCKET NUMBER: 36607-B-PCT-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 2, Application US/07852260 Patent No. 5525715 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2206 amino acids
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Best Local Similarity 36.28
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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Query Match

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US-09-134-001C-2873
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US-09-045-201A-2
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Sequence 15, Application US/09058489

Setent No. 6103886

GENERAL INFORMATION:

APPLICANT: Whitehead Institute for Biomedical Research

APPLICANT: Lahn, Bruce

APPLICANT: Page, David

TITLE OF INVENTION: the Y Chromosome

TITLE OF INVENTION: the Y Chromosome

TITLE OF INVENTION: the Y CALOMOSOME

CURRENT APPLICATION NUMBER: US/09/058,489

CURRENT APPLICATION NUMBER: 60/041,877

EARLIER APPLICATION NUMBER: 60/041,877

SARLIER FILING DATE: 1997-04-11

NUMBER OF SEQ ID NOS: 91

CONTINUED TO SETSEQ FOR Windows Version 3.0
                                                                                        2 NVEH-EVNLL------VEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/09058489
Fatent No. 6103886
GENERAL INFORMATION:
APPLICANT: Whitehead Institute for Biomedical Research
APPLICANT: Lahn, Bruce
APPLICANT: Page, David
TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
TITLE OF INVENTION: the Y Chromosome
FILE REFERENCE: WHI97-08pA
CURRENT APPLICATION NUMBER: US/09/058,489
CURRENT APPLICATION NUMBER: 60/041,877
EARLIER FILING DATE: 1998-04-11
WUMBER OF SED ID NOS: 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 662;
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;; Score 61; DB 4; Length 323;
;; Pred. No. 3.8;
13; Mismatches 27; Indels
                                     27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
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; Pred. No. 20;
12; Mismatches
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                                                                                                                                       52 AAKRKIVTYAGELLLQGVHDDVDIVLLQ 80
                                                                                                                                                                     71 VAKER--VTEWG--TLNGVMVPLEIVLLE 95
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         Best Local Similarity 32.6 Matches 29; Conservative
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Best Local Similarity 28.88
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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US-09-058-489-16
                                                                                                                                                                                                                                  RESULT 3
US-09-058-489-15
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LENGTH: 662
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GENERAL INFORMATION:

APPLICANT: LYON DOUGET te-Stamm et al

APPLICANT: LYON DOUGET ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCY

TITLE OF INVENTION: DEPERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 2873

LENTH: 208
                            10 LVEEIHRLGSKNADGKLSVKFGVL----FQDDRCANLFEALVGTLKAAKRRIVTYAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 MVRRCHSI--REAARRINVASSAVNRQILKLEDEMGATLFDRLPGGLR-----VTAAG 79
2 NVEHEVNL----LVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKR 55
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APPLICANT: Shisheva, Assia
TITLE OF INVENTION: No. 6110718el Mammalian Putative
TITLE OF INVENTION: Phosphatidylinositol-4-Phosphate-5-Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 208;
10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.8%; Score 56; 28.2%; Pred. No.
                                                                                                                                                          Sequence 2873, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/045,201A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09045201A Patent No. 6110718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 ELLLQGVHDDVDIVLLQD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| : : :||||
80 EILTRHI----TLLLQD 92
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. BOX 828
CITY: Bloomfield Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY di
COMPUTER: IBM PC compe
OPERATING SYSTEM: PC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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Best Local Similarity
Matches 22; Conserv
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Query Match
Best Local Similarity 32.6'
Matches 29; Conservative
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CORGANISM: Xenopus laevis
US-09-237-543-6
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CAGANISM: Xenopus laevis
US-09-644-450-6
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Sequence 6, Appli
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Sequence 16, Appl
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                                                                                                       January 17, 2003, 02:04:14; search time 36 Seconds (without alignments) 66.202 Million cell updates/sec
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Sequence
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1 MNVEHEVNLLVEEIHRLGSK.....AGELLLQGVHDDVDIVLLQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-058-489-15
US-09-058-489-16
US-09-134-001C-2873
US-09-045-201A-2
US-09-619-062-2
US-09-619-062-2
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S-08-203-905B-14
S-09-134-001C-4164
S-09-058-489-18
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5-09-347-801-16
5-08-914-375C-60
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -08-981-527A-11
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-08-909-984A-2
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-08-952-127-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-237-543-6
                                                                                                                                                                                                                                                                                                                 262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0 .seq length: 2000000000
                                                                                                                                                                                    US-09-648-310-2
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Match Length
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Maximum DB
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        Sequence 5, Appliance 5, Ap
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ALIGNMENTS

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Search completed: January 17, 2003, 02:19:49
Job time : 73 secs
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (150); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1158
           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kathariou, Sophia
APPLICANT: Lei, Xiang-Heis
TITLE OF INVENTION: Serotype-Specific Probes for Listeria Monocytogenes
FILE REFERENCE: A65378/RFT/DSS
CURRENT APPLICATION NUMBER: US/09/115,150
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 EBEINKLGYEVYQNEYKNATGKDAVSYNEYKR--RIDDSTNPLISISKAPSLKKITDSIY 462
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                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            4 EHEVNLLVEEIHRLGSKNADGKLSVKFGVLFQDDRCANLFEALVGTLKAAKRRKIV--TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::| .:::: | :| |||:| :| :| :| :| || || 51 YKVREIIQKLMLDGDRNKDGKISFDEFVYIFQEVKSSDIAK----TFRKAINRK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 HEVNLLVEEIHRLGSKNADGKLSV-KFGVLFQDDRCANLFEALVGTLKAAKRRK 57
                                                                                                                                                                                                                                                                                                                                                             Length 549;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1158, Application US/09925301

Sequence 1158, Application US/09925301

Sequence 1158, Application US/09925301

SEDERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1158

LENGTH: 639
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.4%; Score 54.5; Dilarity 25.9%; Pred. No. 56; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Score 54.5;
Pred. No. 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09817514A
patent No. US20020078478A1
GENERAL INFORMATION:
APPLICANT: ffrench-Constant, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 AKTTNEWONYLLKGA---IPLVLL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 A-----GELLLQGVHDDVDIVLL 79
                                                                                                                                                                                                                                                                                                                                                         13.4%;
                                                                                                                                                                                                                                                                                                                                                    Query Match 13.49
Best Local Similarity 29.89
Matches 25; Conservative
Patent No. US20010055759A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                   ; ORGANISM: Bacterial US-09-115-150-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-925-301-1158
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                                                                                                                                                                                                                                          LENGTH: 549
TYPE: PRT
                                                                                                                                                                                                                       SEQ ID NO 4
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Gaps
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8
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APPLICANT: Rocheleau, Thomas
APPLICANT: Waterfield, Nicholas
APPLICANT: Waterfield, Nicholas
TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
FILE REFERENCE: 61645
CURRENT APPLICATION NUMBER: US/09/817,514A
CURRENT FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/191806
PRIOR PILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2389 ASVSFADLKIREDYPASLGKIRRIKQISVTLPA----LLGPYODVOAIL 2433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 FGVLFQDDRCANLFEALVGTLKAAKRRIVTYAGELLLQGVHDDVDIVL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nicolaides, Nicholas
APPLICANT: Sass, Philip
APPLICANT: Sass, Philip
APPLICANT: Kinzler, Kenneth
APPLICANT: Grasso, Luigi
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Methods for generating hypermutable
TITLE OF INVENTION: Methods for generating hypermutable
TITLE OF INVENTION: Yeast
FILE REFERENCE: 01107.00097
CURRENT APPLICATION NUMBER: US/09/788,657
CURRENT FILING DATE: 2001-02-21
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                           Score 54.5; DB 10;
Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%; Score 54; DB 10; 29.2%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 94;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                            TYPE: PRT CRGANISM: Photorhabdus luminescens US-09-817-514A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-788-657-16
; Sequence 16, Application US/09788657
; Patent No. US20020123149A1
                                                                                                                                                                                                                                                                                                                                                                                              13.4%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.3%
Best Local Similarity 29.2%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.49
Best Local Similarity 23.99
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNVEHEVNL-----
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                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 2516
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LENGTH: 859
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APPLICANT: Smith, Hilda
TITLE OF INVENTION: STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS
FILE REPERENCE: 2183-475.
CURRENT APPLICATION NUMBER: US/09/767,041
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR PILING DATE: 1999-07-19
PRIOR PLILING DATE: 1999-07-22
PRIOR RELING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PRIOR APPLICATION NUMBER: EP98202467.1
PRIOR FILING DATE: 1998-07-22
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATCHTIN VERSION 3.0
SEQ ID NO 10
LENTH: 239
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GENERAL INFORMATION:
APPLICANT ADLER, JON ELLIOT
TITLE OF INVENTION: T2 TESTE RECEPTORS AND GENES ENCODING SAME
FILE REFERENCE: 078003/0279152/RXT
CURRENT APPLICATION NUMBER: US/09/825,882
CURRENT PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN Ver. 2.1
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136 GTVVGLLNIRMVGEASAEGKLELLQKARGHKKSVTAAFEEMKRAGYDGGRIVM 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 239;
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Pred. No. 22;
8; Mismatches
                                                                                       Sequence 10, Application US/09767041
Patent No. US20020055168A1
GENERAL INFORMATION:
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US-09-115-150-4
; Sequence 4, Application US/09115150
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ORGANISM: Streptococcus suis
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Best Local Similarity 42.9%;
Matches 15; Conservative
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Best Local Similarity 24.8%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; OTHER INFORMATION: ORF2Z
US-09.767-041-10
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; ORGANISM: Hor
US-09-825-882-12
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LENGTH: 309
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APPLICANT: Turner, C. Alexander Jr
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Turner, C. Alexander Jr
APPLICANT: Zambrowicz, Brian
TITLE OF INVERTION: No. 10520020038011A1e1 Human Kinases and Polynucleotides Encoding
CURRENT APPLICATION NUMBER: US/09/783,320
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/183,582
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 60/184,014
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PREDICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/20/772
PRIOR APPLICATION NUMBER: 60/20/773
PRIOR PILING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-22-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
13.7%; Score 55.5; D
Best Local Similarity 24.2%; Pred. No. 89;
Matches 16; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 14110.
SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Escherichia coli
US-09-815-242-10047
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ORGANISM: homo sapiens
US-09-783-320-4
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32 VNLKVRPHSIHALMGENGAGKSTLLKCLFGI-YQKDSGTILFQGKEIDFHSAK----- 83
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                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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Pred. No. 27;
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CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-20-16
       NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                  Sequence 10214, Application US/09815242 Patent No. US20020061569A1
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FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Yamamoto, Robert T.
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illarity 32.5%;
Conservative
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US-09-815-242-10214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: Galina, Chestukhina
TITLE OF INVENTION: NOVEL DELTA-ENDOTOXINS AND NUCLEIC ACID SEQUENCES CODING THEREFOR
FILE REFERENCE: S-30913A
CURRENT APPLICATION NUMBER: US/09/756,526A
CURRENT FILING DATE: 2001-01-08
PRIOR PAPLICATION NUMBER: US 60/175,158
PRIOR PLING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEC ID NO 2
LENGTH: 1163
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                                                                                                                                                                                                                                                                                                                                                         14.0%; Score 57; DB 10; Length 1163; ilarity 35.1%; Pred. No. 58; Conservative 11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFRENCE: ELTTRA.011A

FILE REPERENCE: ELTTRA.011A

CURRENT APPLICATION UNBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR PAPLICATION NUMBER: 60/191,078

PRIOR PAPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 10270
SEQ ID NO 10270
LENCTH: 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-27
PRIOR PLILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                           ; ORGANISM: Bacillus thuringiensis US-09-756-526A-2
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Xu, H. Howard
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Zyskind, Judith W.
Wall, Daniel
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Carr, Grant J.
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nes 20; Conserva
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                                                                                                                                                                                                                                                                       TYPE: PRT
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Matches
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18;

Length 506; Indels ŝ

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7 VNLLV--EEIHRLGSKNADGK---LSVKFGVLFQDDRCANLFEALVGTLKAAKRRIVTY 61
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                                                                             DB 10; Length 506
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           26; Indels
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           Mismatches
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CURRENT FILING DATE: 2001-03-21
PRICH APPLICATION NUMBER: 60/191,078
PRICH FILING DATE: 2000-03-21
PRICH APPLICATION NUMBER: 60/206,848
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11757
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-37
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2001-02-16
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        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-815-242-11757
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                                                                                                                                                                       84 -- EALENGISMVHQELNLVL 101
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                                                                                                                                  62 AGELLLQG---VHDDVDIVL 78
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Yamamoto, Robert T
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APPLICANT: Jana, Wojeiechowska
APPLICANT: Evgeny, Lewitin
APPLICANT: Ludmila, Revina
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Zyskind, Judith W.
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           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
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                                                                                                                                                                                                                                     RESULT 4
US-09-815-242-11757
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      26;
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        APPLICANT: Kyle MacBeth
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THE
FILE REPERENCE: 3580/2738865
CURRENT APPLICATION NUMBER: US/09/971,791
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 323
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                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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Pred. No. 20;
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-12
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Laura A. Rudolph-Owen
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
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32.5%;
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Best Local Similarity 32.6%
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                              ORGANISM: Xenopus laevis
US-09-971-791-6
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Best Local Similarity
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LENGTH: 506
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62 MNVDHEVNLLVEEIHRLGSKNADGKLSVKFGVLFRDDKCANLFEALVGTLKAAKRRKIVT 121
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US-09-971-791-6
Sequence 6, Application US/09971791
Patent No. US20020115120A1
GENERAL INFORMATION:
APPLICANT: Rosanna Kapeller-Libermann
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Best Local Similarity
Matches 76; Conserv
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Sequence 5045, Ap
Sequence 11757, A
Sequence 10270, A
Sequence 10210, A
Sequence 10214, A
Sequence 4, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 12, Appli
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                                                                                                                                                                    January 17, 2003, 02:06:44; Search time 71 Seconds (without alignments) 22.678 Million cell updates/sec
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1 MNVEHEVNLLVEETHRLGSK.....AGELLLQGVHDDVDIVLLQD
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-971-791-6
US-09-815-242-5045
US-09-815-242-11757
US-09-815-242-10210
US-09-815-242-10210
US-09-815-242-10210
US-09-815-242-10210
US-09-815-242-10210
US-09-815-242-10210
US-09-815-242-10210
US-09-925-812-150-4
US-09-925-115-150-4
US-09-925-115-150-4
US-09-925-115-150-4
US-09-925-115-1158
US-09-115-1158
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96.1%; 93.8%;

Conservative

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Sequence 60, Appl Sequence 16, Appl Sequence 16, Appl Sequence 2, Appl Sequence 2, Appl Sequence 150, Ap Sequence 151, Appl Sequence 152, Appl Sequence 1623, A Sequence 1623, A Sequence 1623, A Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 5598, A Sequence 5598, A Sequence 22, Appl Sequence 226, Appl	odies
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367 608 608 608 609 609 609 609 609 609 609 609 609 609	1485 1485, Application US/09 No. US20020151681A1 INFORMATION: ANT: Craig Rosen, CANT: Steve Ruben OF INVENTION: Nucleic Acid ERERENEE: PA10. THERENEE: PA10. THE FILING DATE: 2001-08-1 APPLICATION NUMBER: US/ TFILING DATE: 2000-03-08 APPLICATION NUMBER: G0/12 FILING DATE: 1999-03-12 FILING DATE: 1999-03-12 FILING DATE: 2000-03-08 APPLICATION NUMBER: G0/12 FILING DATE: 2000-03-08 H: 142 PRT ISM: HOMO SADIENS
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\$222 \$33 \$222 \$33 \$232 \$33 \$33 \$332 \$33 \$332 \$332	RESULT 1 US-09-925-300-1485 Sequence 1485, Application US/0992530 Patent No. US20020151681A1 GENERAL INFORMATION: APPLICANT: Craig Rosen, APPLICANT: Steve Ruben TITLE OF INVENTION: Nucleic Acids, P FILE REFERENCE: PA101 CURRENT APPLICATION NUMBER: US/09/92 CURRENT FILING DATE: 2001-08-10 PRIOR PRILING DATE: 2000-03-08 PRIOR FILLING DATE: 1999-01 PRIOR FILLING DATE: 1999-01 PRIOR FILLING DATE: 1999-01 SOFTWARE: PATENTING NUMBER: 60/124,270 NUMBER OF SEQ ID NOS: 1890 SOFTWARE: PATENTING OF SEQ ID NOS: 1890
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